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(54) Title: METHODS AND MICROORGANISMS FOR PRODUCTION OF PANTO-COMPOUNDS

(57) Abstract: The present invention features methods of producing panto-compounds (e.g., pantothenate) using microorganisms in which the pantothenate biosynthetic pathway and/or the isoleucine-valine biosynthetic pathway and/or the coenzymeA biosynthetic pathway has been manipulated. Methods featuring ketopantoate reductase overexpressing microorganisms as well as aspartate α -decarboxylase overexpressing microorganisms are provided. Methods of producing panto-compounds in a precursor-independent manner and in high yield are described. Recombinant microorganisms, vectors, isolated nucleic acid molecules, genes and gene products useful in practicing the above methodologies are also provided. The present invention also features a previously unidentified microbial pantothenate kinase gene, *coaX*, as well as methods of producing panto-compounds utilizing microorganisms having modified pantothenate kinase activity. Recombinant microorganisms, vectors, isolated *coaX* nucleic acid molecules and purified CoaX proteins are featured. Also featured are methods for identifying pantothenate kinase modulators utilizing the recombinant microorganisms and/or purified CoaX proteins of the present invention.

METHODS AND MICROORGANISMS FOR PRODUCTION OF PANTO-COMPOUNDS

Background of the Invention

5 Pantothenate, also known as pantothenic acid or vitamin B5, is a member of the B complex of vitamins and is a nutritional requirement for mammals, including livestock and humans (*e.g.*, from food sources, as a water soluble vitamin supplement or as a feed additive). In cells, pantothenate is used primarily for the biosynthesis of coenzyme A (CoA) and acyl carrier protein (ACP). These coenzymes function in the
10 metabolism of acyl moieties which form thioesters with the sulfhydryl group of the 4'-phosphopantetheine portion of these molecules. These coenzymes are essential in all cells, participating in over 100 different intermediary reactions in cellular metabolism.

The conventional means of synthesizing pantothenate (in particular, the bioactive D isomer) is *via* chemical synthesis from bulk chemicals, a process which is hampered
15 by excessive substrate cost as well as the requirement for optical resolution of racemic intermediates (*e.g.*, resolution of DL-pantolactone to obtain D-pantolactone for chemical condensation with β -alanine). Accordingly, researchers have recently looked to bacterial or microbial systems that produce enzymes useful in pantothenate biosynthesis processes (as bacteria are themselves capable of synthesizing pantothenate). In
20 particular, bioconversion processes have been evaluated as a means of favoring production of the D isomer of pantothenic acid, *e.g.*, using microorganisms which selectively hydrolyze a DL-pantothenic acid ester to D-pantothenic acid; microorganisms which selectively decompose L-pantolactone resulting in D-pantolactone alone; and microorganisms which selectively hydrolyze DL-pantolactone
25 to D-pantoic acid.

There is still, however, significant need for improved pantothenate production processes, in particular, for processes requiring reduced quantities of substrates and/or less expensive substrates. To this end, methods of direct microbial synthesis have recently been examined as a means of improving D-pantothenate production. In
30 microbes, pantothenate biosynthesis is a multistep pathway resulting in condensation of pantoate (derived from α -ketoisovalerate) and β -alanine to form D-pantothenate. The isoleucine-valine (*ilv*) pathway biosynthetic enzymes, acetohydroxyacid synthetase (the *ilvBN* or *alsS* gene product), acetohydroxyacid isomeroreductase (the *ilvC* gene product) and dihydroxyacid dehydratase (the *ilvD* gene product) catalyze the conversion of
35 pyruvate to α -ketoisovalerate. The reactions are further catalyzed by the pantothenate (*pan*) pathway biosynthetic enzymes ketopantoate hydroxymethyltransferase (the *panB* gene product), ketopantoate reductase (the *panE* gene product), aspartate- α -

decarboxylase (the *panD* gene product) and pantothenate synthetase (the *panC* gene product).

The genes encoding the enzymes involved in the biosynthesis of pantothenic acid in *Salmonella typhimurium* and *Escherichia coli* have recently been identified and characterized (Frodyma and Downs (1998) *J. Biol. Chem.* 273:5572-5576 and Jackowski (1996) pp. 687-694, In Neidhardt *et al* (ed.) *Escherichia coli* and *Salmonella*: Cellular and Molecular Biology, 2nd ed. Am. Soc. Microbiol. Wash, D.C). In *E. coli*, for example, the biosynthesis of pantothenic acid consists of four key steps. The first reaction is catalyzed by the *panB* gene product, ketopantoate hydroxymethyltransferase, and uses the L-valine intermediate α -ketoisovalerate to generate ketopantoate, which is subsequently reduced to pantoate by the *panE* gene product, ketopantoate reductase. The *panD* gene product, aspartate- α -decarboxylase, generates β -alanine from aspartate. The *panC* gene product, pantothenate synthetase, subsequently ligates β -alanine with pantoate to yield D-pantothenate.

The authors Dusch *et al.* described the identification of the *Corynebacterium glutamicum panD* gene and reported that expression of the *C. glutamicum panD* gene in *E. coli* yielded a strain producing pantothenate with a specific productivity of 140 ng of pantothenate per mg (dry weight) per hour. (Dusch *et al.* (1999) *Appl. Environ. Microbiol.* 65:1530-1539).

The authors Sahm and Eggeling have further identified the *Corynebacterium glutamicum panB* and *panC* genes and have described a genetically engineered strain of *C. glutamicum* which overexpresses the *panBC* genes (Sahm and Eggeling (1999) *Appl. Environ. Microbiol.* 65:1973-1979). The engineered strain produces pantothenate, however, it was necessary to overexpress the genes responsible for α -ketoisovalerate production in the host organism in order that pantothenic acid production could be detected. Moreover, without the addition of β -alanine, no substantial amounts of pantothenate accumulated with the strain constructed.

Likewise, a method of producing D-pantothenic acid has been described that takes advantage of a sodium salicylate resistant mutant strain of *E. coli* which produces D-pantothenic acid when cultured in the presence of β -alanine (U.S. Patent No. 5,518,906). Generation of *E. coli* strains resistant to α -ketoisovaleric acid and/or α -ketobutyric acid, and/or α -aminobutyric acid, and/or β -hydroxyaspartic acid and/or O-methyl-threonine, in addition to salicylic acid, further increased pantothenic acid production. Moreover, transformation of a plasmid DNA carrying the *panB*, *panC* and *panD* genes into the salicylic acid resistant mutant strain resulted in increased pantothenate production, however, up to 20 g/L β -alanine or more was fed in the examples given. The *panB-panC-panD* genes are clustered on the *E. coli* chromosome.

Finally, a method of producing D-pantothenic acid has been described which utilizes a salicylic acid-resistant, α -ketoisovalerate-resistant, α -ketobutyrate-resistant, β -hydroxyaspartate-resistant, o-methylthreonine-resistant *E. coli* strain transformed with pantothenate biosynthesis gene-containing DNA fragments and/or branched amino acid biosynthesis gene-containing DNA fragments and cultured in the presence of β -alanine (U.S. Patent No. 5,932,457).

Pantothenate production in bacteria results from the condensation of pantoate and β -alanine and involves the pantothenate biosynthetic enzymes ketopantoate hydroxymethyltransferase (the *panB* gene product), ketopantoate reductase (the *panE* gene product), aspartate- α -decarboxylase (the *panD* gene product) and pantothenate synthetase (the *panC* gene product). Although pantothenate is biologically active as a vitamin, it is further metabolized in all cells to Coenzyme A (CoA) which participates as an acyl group carrier in the tricarboxylic acid (TCA) cycle, fatty acid metabolism and numerous other reactions of intermediary metabolism. The initial (and possibly rate-controlling) step in the conversion of pantothenate to Coenzyme A (CoA) is phosphorylation of pantothenate by pantothenate kinase. A pantothenate kinase activity was first identified in *Salmonella typhimurium* by screening for temperature-sensitive mutants which synthesized CoA at permissive temperatures but excreted pantothenate at non-permissive temperatures. The mutations were mapped in the *Salmonella* chromosome and the genetic locus was designated *coaA*. The gene encodes the enzyme that catalyzes the first step in the biosynthesis of coenzyme A from pantothenate (Dunn and Snell (1979) *J. Bacteriol.* 140:805-808). *Escherichia coli* temperature sensitive mutants have also been isolated and characterized (Vallari and Rock (1987) *J. Bacteriol.* 169:5795-5800). These mutants (named *coaA15(Ts)*) are defective in the conversion of pantothenate to CoA and further exhibit a temperature-sensitive growth phenotype, indicating that pantothenate kinase activity is essential for growth. Moreover, it was noted that CoA inhibited pantothenate kinase activity to the same degree in the mutant as compared to the wild-type enzyme.

Feedback resistant *E. coli* mutants (named *coaA16(Fr)*) have also been isolated that possess a pantothenate kinase activity that is refractory to feedback inhibition by CoA (Vallari and Jackowski (1988) *J. Bacteriol.* 170:3961-3966). The mutation responsible for the reversion is, surprisingly, not genetically linked to the *coaA* gene by transduction. Additional data described therein support the view that the total cellular CoA content is controlled by both modulation of biosynthesis at the pantothenate kinase step and possibly by degradation of CoA to 4'-phosphopantetheine.

The wild-type *E. coli coaA* gene was cloned by functional complementation of *E. coli* temperature-sensitive mutants. The sequence of the wild-type gene was determined (Song and Jackowski (1992) *J. Bacteriol.* 174:6411-6417 and Flamm *et al.* (1988) *Gene (Amst.)* 74:555-558). Strains containing multiple copies of the *coaA* gene possessed 76-fold higher specific activity of pantothenate kinase, however, there was only a 2.7-fold increase in the steady state level of CoA (Song and Jackowski, *supra*). It has further been reported that the prokaryotic enzyme (encoded by *coaA* in *E. coli* and a variety of other microorganisms) is feedback inhibited by CoA both *in vivo* and *in vitro* with CoA being about five times more potent than acetyl-CoA in inhibiting the enzyme (Song and Jackowski, *supra* and Vallari *et al.*, *supra*). Moreover, it has been reported that the *panB* gene product in *E. coli* is inhibited by CoA (Powers and Snell (1976) *J. Biol. Chem.* 251:3786-3793). These data further support the view that feedback inhibition of pantothenate kinase activity is a critical factor controlling intracellular CoA concentration.

Using standard search and alignment tools, *coaA* homologues have been identified in *Hemophilus influenzae*, *Mycobacterium tuberculosis*, *Vibrio cholerae*, *Streptococcus pyogenes* and *Bacillus subtilis*. By contrast, proteins with significant similarity could not be identified in eukaryotic cells including *Saccharomyces cerevisiae* or in mammalian expressed sequence tag (EST) databases. Using a genetic selection strategy, a cDNA encoding pantothenate kinase activity has recently been identified from *Aspergillus nidulans* (Calder *et al.* (1999) *J. Biol. Chem.* 274:2014-2020). The eukaryotic pantothenate kinase gene (*panK*) has distinct primary structure and unique regulatory properties that clearly distinguish it from its prokaryotic counterpart. A mammalian pantothenate kinase gene (*mpanK1a*) has also been isolated which encodes a protein having homology to the *A. nidulans* PanK protein and to the predicted gene product of GenBank™ Accession Number 927798 identified in the *S. cerevisiae* genome (Rock *et al.* (2000) *J. Biol. Chem.* 275:1377-1383).

Summary of the Invention

The present invention is based, at least in part, on the discovery of key enzyme-encoding genes of the pantothenate biosynthetic pathway in *Bacillus subtilis*. In particular, the present inventors have identified the *panE* gene of *B. subtilis*. Overexpression or deregulation of the *panE* gene in *B. subtilis* results in enhanced production of the *panE* gene product, ketopantoate reductase, further resulting in increased production of pantothenate. Likewise, mutations in this gene reduce pantothenate production in *B. subtilis* >90%. The present inventors have further identified the presumptive *panBCD* operon in *B. subtilis*, overexpression or

deregulation of which results in increased pantothenate production. The present inventors have further demonstrated that overexpression or deregulation of the *panD* gene in *B. subtilis* (resulting in enhanced production of the *panD* gene product, aspartate- α -decarboxylase) further results in increased production of pantothenate, in particular, in combination with deregulation of genes encoding key enzymes of the isoleucine-valine (*ilv*) biosynthetic pathway.

Accordingly, the present invention features methods of producing pantothenate, as well as other compounds of the pantothenate biosynthetic pathway (*e.g.*, ketopantoate, pantoate and β -alanine), termed "panto-compounds" herein, using microorganisms in which the pantothenate biosynthetic pathway and/or isoleucine-valine biosynthetic pathway has been manipulated such that pantothenate or other desired panto-compounds are produced. In one embodiment, the invention features a method of producing a panto-compound (*e.g.*, pantothenate or pantoate) that involves culturing a microorganism which overexpresses the *panE* gene product, ketopantoate reductase, also referred to herein as a ketopantoate reductase-overexpressing or "KPAR-O" microorganism, under conditions such that the panto-compound (*e.g.*, pantothenate or pantoate) is produced. In another embodiment, the present invention features a method of producing panto-compounds (*e.g.*, pantothenate or pantoate) which includes culturing a microorganism which overexpresses at least one pantothenate biosynthetic enzyme (*e.g.*, at least one of the *panB*, *panC* or *panD* gene products), preferably in a KPAR-O microorganism, under conditions such that the panto-compound (*e.g.*, pantothenate or pantoate) is produced.

Yet another aspect of the invention features methods of producing panto-compounds which are independent of the need to feed precursors (*e.g.*, β -alanine or aspartate and/or α -ketoisovalerate or valine). In one embodiment, the invention features a method of producing pantothenate in a manner independent of precursor feed that includes culturing an aspartate- α -decarboxylase-overexpressing (A α D-O) microorganism having a deregulated isoleucine-valine (*ilv*) pathway under conditions such that pantothenate is produced. In another embodiment, the invention features a method of producing pantothenate in a manner independent of precursor feed that includes culturing an A α D-O microorganism having a deregulated pantothenate (*pan*) pathway and a deregulated isoleucine-valine (*ilv*) pathway, under conditions such that pantothenate is produced. In another embodiment, the invention features a method of producing pantothenate in a manner independent of aspartate or β -alanine feed that includes culturing an A α D-O microorganism under conditions such that pantothenate is produced. In another embodiment, the invention features a method of producing pantothenate in a manner independent of valine or α -ketoisovalerate feed that includes

culturing a microorganism having a deregulated isoleucine-valine (*ilv*) biosynthetic pathway under conditions such that pantothenate is produced. In yet another embodiment, the invention features a high yield production method for producing pantothenate that includes culturing a manipulated microorganism under conditions
5 such that pantothenate is produced at a significantly high yield (e.g., at a level greater than 10 g/L, 20 g/L, 30 g/L or 40g/L).

The methods of the present invention further feature microorganisms that overexpresses acetohydroxyacid synthetase or acetohydroxyacid isomeroreductase (e.g., microorganisms transformed with a vector that includes an *ilvBNC* nucleic acid
10 sequence), microorganisms that overexpresses dihydroxyacid dehydratase (e.g., microorganisms transformed with a vector that includes an *ilvD* nucleic acid sequence), microorganisms that overexpresses aspartate- α -decarboxylase (e.g., microorganisms transformed with a vector that includes a *panD* nucleic acid sequence), microorganisms having a deregulated isoleucine-valine (*ilv*) biosynthetic pathway and microorganisms
15 having a deregulated pantothenate biosynthetic pathway (e.g., microorganisms that overexpress any of ketopantoate hydroxymethyltransferase, ketopantoate reductase, pantothenate synthetase and aspartate- α -decarboxylase, for example, microorganisms transformed with a vector comprising a *panBCD* nucleic acid sequence or a vector comprising a *panEI* nucleic acid sequence). In one embodiment, the recombinant
20 microorganism is Gram positive (e.g., microorganisms belonging to the genus *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*). In another embodiment, the recombinant microorganism is Gram negative. Particularly preferred is a *Bacillus* recombinant microorganism (e.g., *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus subtilis*, *Bacillus pumilus*, *Bacillus halodurans*, and the like). Recombinant
25 vectors that contain the genes encoding *Bacillus* pantothenate and/or isoleucine-valine biosynthetic enzymes (e.g., *B. subtilis* pantothenate and/or isoleucine-valine biosynthetic enzymes) are also described.

Also featured are methods of producing β -alanine that include culturing an aspartate- α -decarboxylase-overexpressing (A α D-O) microorganism under conditions
30 such that β -alanine is produced and methods of producing β -alanine that involve contacting a composition comprising aspartate with an isolated *Bacillus* aspartate- α -decarboxylase enzyme under conditions such that β -alanine is produced.

The production methods of the present invention further can include recovering the panto-compound (e.g., pantothenate or pantoate).

35 The present invention further features recombinant microorganisms (e.g., A α D-O microorganisms, microorganisms having a deregulated isoleucine-valine (*ilv*) pathway, microorganisms overexpressing at least one of ketopantoate

hydroxymethyltransferase (the *panB* gene product), pantothenate synthetase (the *panC* gene product), aspartate- α -decarboxylase (the *panD* gene product), ketopantoate reductase (the *panE1* gene product) and microorganisms having a deregulated *panBCD* operon. Also featured are *panB*, *panC*, *panD*, *panE*, *ilvB*, *ilvN*, *alsS*, *ilvC*, and/or *ilvD* nucleic acid molecules, as well as vectors including such nucleic acid molecules and gene products encoded by such nucleic acid molecules.

The methodology of the present invention further includes, for example in addition to overexpressing at least one pantothenate biosynthetic enzyme, deleting or mutating a second pantothenate biosynthetic enzyme, said second pantothenate biosynthetic enzyme preferably being downstream of the desired product in the pantothenate biosynthetic pathway. For example, mutating *panC*, in addition to overexpressing the *panE* gene product, results in even further enhanced or increased production of pantoate. Accordingly, in one embodiment, the invention features a method of producing pantoate which includes culturing a microorganism which overexpresses the *panE* gene product and which has a deletion in the *panC* gene. In another embodiment, the invention features a method of producing pantoate which includes culturing a microorganism which overexpresses the *panE* gene product and/or *panB* gene product and which has a deletion in the *panC* gene. Other exemplary embodiments include a method of producing ketopantoate which includes culturing a microorganism which overexpresses the *panB* gene product and which has a deletion in the *panE* gene and a method of producing β -alanine which includes culturing a microorganism which overexpresses the *panD* gene product and which has a deletion in the *panC* gene. Also included are methods of producing panto-compounds which include overexpressing at least one valine biosynthetic enzyme in a microorganism which has at least one pantothenate biosynthetic enzyme deleted.

The present invention is also based at least in part, on the identification and characterization of a previously unidentified microbial pantothenate kinase gene, *coaX*. *CoaX* was first identified in *Bacillus subtilis* and corresponds to an open reading frame in a portion of the chromosomal DNA that includes the 5' end of the *ftsH* gene, and all of the *yacB*, *yacC*, *yacD*, *cysK* and *pabB* genes. The present inventors have demonstrated that the *yacB* open reading frame encodes a novel pantothenate kinase activity, the gene being unrelated by homology to any previously known pantothenate kinase gene. The gene has been renamed *coaX*, as it encodes the enzyme which catalyzes the first step in the pathway from pantothenate to CoaA.

Accordingly, the present invention features new and improved methods of producing pantothenate and other key compounds of the pantothenate biosynthetic pathway (e.g., panto-compounds) utilizing microorganisms having modified

pantothenate kinase activity. In particular, the present invention features recombinant microorganisms that contain the *coaX* gene or that contain a mutant *coaX* gene, having reduced pantothenate kinase activity. In one embodiment, the invention features such recombinant microorganisms further having a deregulated pantothenate biosynthetic pathway. In another embodiment, the invention features such recombinant microorganisms further having a deregulated isoleucine-valine (*ilv*) pathway. In a preferred embodiment, the microorganisms belong to the genus *Bacillus* (e.g., *B. subtilis*).

The present invention also features recombinant microorganisms (e.g., microorganisms belonging to the genus *Bacillus*, for example, *B. subtilis*) that contain the *coaA* gene or that contain a mutant *coaA* gene, optionally including a *coaX* gene or mutant thereof, having reduced pantothenate kinase activity. In one embodiment, the invention features such recombinant microorganisms further having a deregulated pantothenate biosynthetic pathway or having a deregulated isoleucine-valine (*ilv*) pathway.

Also featured are vectors that contain isolated *coaX* or *coaA* genes as well as mutant *coaX* and/or *coaA* genes. Isolated nucleic acid molecules that contain isolated *coaX* genes or mutant *coaX* genes are featured in addition to isolated CoaX proteins and mutant CoaX proteins.

The nucleic acids, vectors and recombinant microorganisms described above are particularly useful in the methodologies of the present invention. In particular, the invention features methods of enhancing panto-compound production (e.g., ketopantoate, pantoate and or pantothenate production) that include culturing a recombinant microorganism having a mutant *coaX* gene under conditions such that panto-compound production is enhanced. In one embodiment, the recombinant microorganism further includes a mutant *coaA* gene. In another embodiment, the recombinant microorganism further includes a mutant *avtA* and/or mutant *ilvE* gene and/or mutant *ansB* gene and/or mutant *alsD* gene. Also featured are methods for identifying pantothenate modulators utilizing the recombinant microorganisms and purified CoaX proteins of the present invention.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

Brief Description of the Drawings

Figure 1 is a schematic representation of the pantothenate biosynthetic pathway.

Figure 2 is a schematic representation of the plasmid pAN240, containing sequences ligated upstream of the $P_{26}panBCD$ cassette, equivalent to the integrated version in strain PA221.

Figure 3A is a schematic representation of the plasmid pAN004, containing the *panBCD* operon expressed from P_{26} and RBS1.

Figure 3B is a schematic representation of the plasmid pAN006, containing the *panBCD* operon expressed from P_{26} and RBS2.

Figure 4 is a schematic representation of the plasmid pAN236, containing an integratable and amplifiable P_{26} -RBS2-*panE1* expression cassette.

Figure 5 is a schematic representation of the construction of plasmid pAN423.

Figure 6 is a schematic representation of the construction of plasmids pAN426 and pAN427.

Figure 7 is a schematic representation of the construction of plasmids pAN428 and pAN429.

Figure 8 is a schematic representation of the construction of plasmid pAN431.

Figure 9 is a schematic representation of the construction of plasmid pAN441.

Figure 10 is a schematic representation of the construction of plasmid pAN440.

Figure 11 is a schematic representation of the plasmid pAN251 designed to integrate a single copy of a P_{26} -*panE1* cassette at the *panE1* locus by double crossover.

Figure 12 is a schematic representation of the plasmid pAN267 designed to integrate a single copy of a P_{26} -*ilvBNC* cassette at the *amyE* locus.

Figure 13 is a schematic representation of the plasmid pAN257, a clone of *Bacillus subtilis ilvD* in a low copy vector.

Figure 14 is a schematic representation of the plasmid pAN263, designed to integrate a single copy of a P_{26} -*ilvD* cassette at the *ilvD* locus.

Figure 15 is a schematic representation of the plasmid pAN261, designed to disrupt the *Bacillus subtilis ilvD* gene with the *cat* gene.

Figure 16 is a schematic representation of the Coenzyme A biosynthetic pathway in *E. coli*.

Figure 17 is a schematic representation of the structure of pAN296, a plasmid designed to delete most of the *B. subtilis coaA* gene and substitute a chloramphenicol resistance gene.

Figure 18 is a schematic representation of the structure of the *Bacillus subtilis* genome in the region of the *coaA* gene. The scale is in base pairs and the significant open reading frames are shown by open arrows.

Figure 19 is a schematic representation of the plasmid pAN281, a plasmid for expressing *Bacillus subtilis* *coaA* after integration at the *bpr* locus.

Figure 20A-B depicts a multiple sequence alignment (MSA) of the amino acid sequences encoded by six known or predicted microbial *coaA* genes. SEQ ID NOs:4-6 and 1-3 correspond to the amino acid sequences of *Mycobacterium leprae* (SwissProt™ Accession No. Q9X795), *Mycobacterium tuberculosis* (SwissProt™ Accession No. O53440), *Streptomyces coelicolor* (SwissProt™ Accession No. O86799), *Haemophilus influenzae* (SwissProt™ Accession No. P44793), *Escherichia coli* SwissProt™ Accession No. P15044) and *Bacillus subtilis* (SwissProt™ Accession No. P54556), respectively. The alignment was generated using ClustalW MSA software at the GenomeNet CLUSTALW Server at the Institute for Chemical Research, Kyoto University. The following parameters were used: Pairwise Alignment, K-tuple (word) size = 1, Window size = 5, Gap Penalty = 3, Number of Top Diagonals = 5, Scoring Method = Percent; Multiple Alignment, Gap Open Penalty = 10, Gap Extension Penalty = 0.0, Weight Transition = No, Hydrophilic residues = Gly, Pro, Ser, Asn, Asp, Gln, Glu, Arg and Lys, Hydrophobic Gaps = Yes; and Scoring Matrix = BLOSUM.

Figure 21 is a schematic representation of the structure of the *Bacillus subtilis* genome in the region of the *coaX* (*yacB*) gene. The scale is in base pairs, the significant open reading frames are shown by open arrows and certain predicted restriction fragments are indicated by thick bars.

Figure 22 is a schematic representation of the structure of pAN341 and pAN342, two independent PCR-derived clones of *B. subtilis* *yacB* (remained herein as *coaX*).

Figure 23A-D depicts a multiple sequence alignment (MSA) of the amino acid sequences encoded by fourteen known or predicted microbial *coaX* genes. SEQ ID NOs:9, 74, 7-8, 75, 11, 10 and 12-18 correspond to the amino acid sequences of *Bacillus subtilis* (SwissProt™ Accession No. P37564), *Clostridium acetobutylicum* (WIT™ Accession No. RCA03301, Argonne National Laboratories), *Streptomyces coelicolor* (PIR™ Accession No. T36391), *Mycobacterium tuberculosis* (SwissProt™ Accession No. O06282), *Rhodobacter capsulatus* (WIT™ Accession No. RRC02473), *Desulfovibrio vulgaris* (DBJ™ Accession No. BAA21476.1), *Deinococcus radiodurans* (SwissProt™ Accession No. Q9RX54), *Thermotoga maritima* (GenBank™ Accession No. AAD35964.1), *Treponema pallidum* (SwissProt™ Accession No. O83446), *Borrelia burgdorferi* (SwissProt™ Accession No. O51477), *Aquifex aeolicus* (SwissProt™ Accession No. O67753), *Synechocystis* sp. (SwissProt™ Accession No. P74045), *Helicobacter pylori* (SwissProt™ Accession No. O25533), and *Bordetella pertussis* (SwissProt™ Accession No. Q45338), respectively. The alignment was generated using ClustalW MSA software at the GenomeNet CLUSTALW Server at the

Institute for Chemical Research, Kyoto University. The following parameters were used: Pairwise Alignment, K-tuple (word) size = 1, Window size = 5, Gap Penalty = 3, Number of Top Diagonals = 5, Scoring Method = Percent; Multiple Alignment, Gap Open Penalty = 10, Gap Extension Penalty = 0.0, Weight Transition = No, Hydrophilic residues = Gly, Pro, Ser, Asn, Asp, Gln, Glu, Arg and Lys, Hydrophobic Gaps = Yes; and Scoring Matrix = BLOSUM.

Figure 24 depicts a multiple sequence alignment of a portion of the protein sequences of the *coaA* gene products from the following microorganisms: *Bacillus subtilis*, *Escherichia coli*, *Haemophilus influenzae*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, and *Streptomyces coelicolor*. The residues that are mutated in *E. coli coaA15(Ts)* and *B. subtilis coaA282A* are indicated below and above the alignment, respectively. The portions correspond to amino acid residues 168-187 of SEQ ID NO:3, 167-186 of SEQ ID NO:2, 165-184 of SEQ ID NO:1, 169-188 of SEQ ID NO:4, 169-188 of SEQ ID NO:5 and 179-198 of SEQ ID NO:6, respectively.

Figure 25 is a schematic representation of the structure of pAN294, a plasmid for integrating mutagenized *B. subtilis coaA* at its native locus.

Figure 26 is a schematic representation of the structure of pAN336, a plasmid designed to delete *B. subtilis coaX* from its chromosomal locus and replace it with a kanamycin resistance gene.

Detailed Description of the Invention

The present invention features new and improved methods of producing pantothenate and other key compounds of the pantothenate biosynthetic pathway (referred to herein as "panto-compounds", for example, pantothenate, ketopantoate, pantoate and β -alanine) using microorganisms in which the pantothenate biosynthetic pathway has been manipulated such that pantothenate or other desired panto-compounds are produced.

The new and improved methodologies of the present invention include methods of producing panto-compounds (e.g., pantothenate) in microorganisms having at least one enzyme of the pantothenate biosynthetic pathway manipulated such that pantothenate or other desired panto-compounds are produced (e.g., produced at an increased level). For example, the invention features methods of producing panto-compounds (e.g., pantothenate) in microorganisms having at least one of ketopantoate hydroxymethyltransferase, ketopantoate reductase, pantothenate synthetase or aspartate- α -decarboxylase manipulated such that pantothenate or other desired panto-compounds are produced. The methodologies of the present invention also include methods of producing panto-compounds (e.g., pantothenate) in microorganisms having at least one

valine-isoleucine biosynthetic enzyme, described herein, manipulated such that pantothenate or other desired panto-compounds are produced. For example, the invention features methods of producing panto-compounds (*e.g.*, pantothenate) in microorganisms having at least one of acetohydroxyacid synthetase, acetohydroxyacid isomeroreductase or dihydroxyacid dehydratase manipulated such that pantothenate or other desired panto-compounds are produced.

The invention also features methods of producing panto-compounds that involve culturing a ketopantoate reductase-overexpressing (KPAR-O) microorganism under conditions such that the panto-compound is produced. The invention also features methods of producing pantothenate in a manner independent of precursor feed that involve culturing an aspartate- α -decarboxylase-overexpressing (A α D-O) microorganism under conditions such that pantothenate is produced. Also featured are β -alanine independent high yield pantothenate production methods as well as methods of producing β -alanine. The present invention also features methods for enhancing production of panto-compounds that involve culturing pantothenate kinase mutants. In particular, the present invention features new and improved methods of producing pantothenate and other key compounds of the pantothenate biosynthetic pathway (*e.g.*, panto-compounds) utilizing microorganisms having modified pantothenate kinase activity, for example, microorganisms that include the *coaX* gene or that include a mutant *coaX* gene, having reduced pantothenate kinase activity.

In order that the present invention may be more readily understood, certain terms are first defined herein.

The term "pantothenate biosynthetic pathway" includes the biosynthetic pathway involving pantothenate biosynthetic enzymes (*e.g.*, polypeptides encoded by biosynthetic enzyme-encoding genes), compounds (*e.g.*, precursors, substrates, intermediates or products), cofactors and the like utilized in the formation or synthesis of pantothenate. The term "pantothenate biosynthetic pathway" includes the biosynthetic pathway leading to the synthesis of pantothenate in a microorganisms (*e.g.*, *in vivo*) as well as the biosynthetic pathway leading to the synthesis of pantothenate *in vitro*. Figure 1 includes a schematic representation of the pantothenate biosynthetic pathway. Pantothenate biosynthetic enzymes are depicted in bold and their corresponding genes indicated in italics.

The term "pantothenate biosynthetic enzyme" includes any enzyme utilized in the formation of a compound (*e.g.*, intermediate or product) of the pantothenate biosynthetic pathway. According to Figure 1, synthesis of pantoate from α -ketoisovalerate (α -KIV) proceeds *via* the intermediate, ketopantoate. Formation of ketopantoate is catalyzed by the pantothenate biosynthetic enzyme ketopantoate

hydroxymethyltransferase (the *panB* gene product). Formation of pantoate is catalyzed by the pantothenate biosynthetic enzyme ketopantoate reductase (the *panE* gene product). Synthesis of β -alanine from aspartate is catalyzed by the pantothenate biosynthetic enzyme aspartate- α -decarboxylase (the *panD* gene product). Formation of
5 pantothenate from pantoate and β -alanine (*e.g.*, condensation) is catalyzed by the pantothenate biosynthetic enzyme pantothenate synthetase (the *panC* gene product).

The term "isoleucine-valine biosynthetic pathway" includes the biosynthetic pathway involving isoleucine-valine biosynthetic enzymes (*e.g.*, polypeptides encoded by biosynthetic enzyme-encoding genes), compounds (*e.g.*, precursors, substrates,
10 intermediates or products), cofactors and the like utilized in the formation or synthesis of conversion of pyruvate to valine or isoleucine. The term "isoleucine-valine biosynthetic pathway" includes the biosynthetic pathway leading to the synthesis of valine or isoleucine in a microorganisms (*e.g.*, *in vivo*) as well as the biosynthetic pathway leading to the synthesis of valine or isoleucine *in vitro*. Figure 1 includes a
15 schematic representation of the isoleucine-valine biosynthetic pathway. Isoleucine-valine biosynthetic enzymes are depicted in bold italics and their corresponding genes indicated in italics

The term "isoleucine-valine biosynthetic enzyme" includes any enzyme utilized in the formation of a compound (*e.g.*, intermediate or product) of the isoleucine-valine
20 biosynthetic pathway. According to Figure 1, synthesis of valine from pyruvate proceeds *via* the intermediates, acetolactate, α,β -dihydroxyisovalerate (α,β -DHIV) and α -ketoisovalerate (α -KIV). Formation of acetolactate from pyruvate is catalyzed by the isoleucine-valine biosynthetic enzyme acetohydroxyacid synthetase (the *ilvBN* gene product, or alternatively, the *alsS* gene product). Formation of α,β -DHIV from
25 acetolactate is catalyzed by the isoleucine-valine biosynthetic enzyme acetohydroxyacidisomero reductase (the *ilvC* gene product). Synthesis of α -KIV from α,β -DHIV is catalyzed by the isoleucine-valine biosynthetic enzyme dihydroxyacid dehydratase (the *ilvD* gene product). Moreover, valine and isoleucine can be interconverted by branched chain amino acid transaminases.

30 As used herein, each of ketopantoate, pantoate, β -alanine and pantothenate are "panto-compounds". The term "panto-compound" includes a compound (*e.g.*, a substrate, intermediate or product) in the pantothenate biosynthetic pathway which is downstream from a particular pantothenate biosynthetic enzyme. In one example, a panto-compound is downstream of the pantothenate biosynthetic enzyme ketopantoate
35 hydroxymethyltransferase (the *panB* gene product) and can include ketopantoate, pantoate and/or pantothenate. In another example, a panto-compound is downstream of the pantothenate biosynthetic enzyme ketopantoate reductase (the *panE* gene product)

and can include pantoate and/or pantothenate. In yet another example, a panto-compound is downstream of the pantothenate biosynthetic enzyme pantothenate synthetase (the *panC* gene product) and can include pantothenate. In yet another example, a panto-compound is downstream of the pantothenate biosynthetic enzyme aspartate- α -decarboxylase (the *panD* gene product) and can include β -alanine and/or pantothenate.

Preferred panto-compounds include pantothenate and pantoate. The term "pantothenate" includes the free acid form of pantothenate, also referred to as "pantothenic acid" as well as any salt thereof (*e.g.*, derived by replacing the acidic hydrogen of pantothenate or pantothenic acid with a cation, for example, calcium, sodium, potassium, ammonium), also referred to as a "pantothenate salt". The term "panto-compound" also includes alcohol derivatives of pantothenate. Preferred pantothenate salts are calcium pantothenate or sodium pantothenate. A preferred alcohol derivative is pantothenol. Pantothenate salts and/or alcohols of the present invention include salts and/or alcohols prepared *via* conventional methods from the free acids described herein. In another embodiment, calcium pantothenate is synthesized directly by a microorganism of the present invention. A pantothenate salt of the present invention can likewise be converted to a free acid form of pantothenate or pantothenic acid by conventional methodology.

The term "pantoate" includes the free acid form of pantoate, also referred to as "pantoic acid" as well as any salt thereof (*e.g.*, derived by replacing the acidic hydrogen of pantoate or pantoic acid with a cation, for example, calcium, sodium, potassium, ammonium), also referred to as a "pantoate salt". Preferred pantoate salts are calcium pantoate or sodium pantoate. Pantoate salts of the present invention include salts prepared *via* conventional methods from the free acids described herein. A pantoate salt of the present invention can likewise be converted to a free acid form of pantoate or pantoic acid by conventional methodology. Moreover, a free acid form of pantoate or pantoic acid can be converted to pantolactone by conventional methodology.

The term "CoA biosynthetic pathway" includes the biosynthetic pathway involving CoA biosynthetic enzymes (*e.g.*, polypeptides encoded by biosynthetic enzyme-encoding genes), compounds (*e.g.*, precursors, substrates, intermediates or products), cofactors and the like utilized in the formation or synthesis of CoA from pantothenate. A schematic representation of the CoA biosynthetic pathway in *E. coli* is set forth as Figure 16. (The pathway depicted is also presumed to be that utilized by other microorganisms.) The term "CoA biosynthetic pathway" includes the biosynthetic pathway leading to the synthesis of CoA in microorganisms (*e.g.*, *in vivo*) as well as the biosynthetic pathway leading to the synthesis of CoA *in vitro*. The term "Coenzyme A

or CoA biosynthetic enzyme" includes any enzyme utilized in the formation of a compound (e.g., intermediate or product) of the CoA biosynthetic pathway, for example, the *coaA*, *panK* or *coaX* gene product which catalyzes the phosphorylation of pantothenate to form 4'-phosphopantothenate, or the *coaD* gene product which catalyzes the conversion of 4'-phosphopantetheine to dephosphocoenzyme A.

I. Recombinant Microorganisms and Methods for Culturing Microorganisms Such That Panto-Compounds are Produced

The methodologies of the present invention feature microorganisms, e.g., recombinant microorganisms, preferably including vectors or genes (e.g., wild-type and/or mutated genes) as described herein and/or cultured in a manner which results in the production of a desired product (e.g. a panto-compound or panto-compounds). The term "recombinant" microorganism includes a microorganism (e.g., bacteria, yeast cell, fungal cell, etc.) which has been genetically altered, modified or engineered (e.g., genetically engineered) such that it exhibits an altered, modified or different genotype and/or phenotype (e.g., when the genetic modification affects coding nucleic acid sequences of the microorganism) as compared to the naturally-occurring microorganism from which it was derived. Preferably, a "recombinant" microorganism of the present invention has been genetically engineered such that it overexpresses at least one bacterial gene or gene product (e.g., a pantothenate or isoleucine-valine biosynthetic enzyme encoding-gene) as described herein, preferably a biosynthetic enzyme encoding-gene included within a recombinant vector as described herein and/or a biosynthetic enzyme expressed from a recombinant vector. The ordinary skilled will appreciate that a microorganism expressing or overexpressing a gene product produces or overproduces the gene product as a result of expression or overexpression of nucleic acid sequences and/or genes encoding the gene product.

The term "manipulated microorganism" includes a microorganism that has been engineered (e.g., genetically engineered) or modified such that the microorganism has at least one enzyme of the pantothenate biosynthetic pathway and/or at least one enzyme of the isoleucine-valine biosynthetic pathway modified such that pantothenate or other desired panto-compounds are produced. Modification or engineering of such microorganisms can be according to any methodology described herein including, but not limited to, deregulation of a biosynthetic pathway and/or overexpression of at least one biosynthetic enzyme. A "manipulated" enzyme (e.g., a "manipulated" biosynthetic enzyme) includes an enzyme, the expression or production of which has been altered or modified such that at least one upstream or downstream precursor, substrate or product

of the enzyme is altered or modified, for example, as compared to a corresponding wild-type or naturally occurring enzyme.

The term "overexpressed" or "overexpression" includes expression of a gene product (*e.g.*, a pantothenate biosynthetic enzyme or isoleucine-valine biosynthetic enzyme) at a level greater than that expressed prior to manipulation of the microorganism or in a comparable microorganism which has not been manipulated. In one embodiment, the microorganism can be genetically manipulated (*e.g.*, genetically engineered) to overexpress a level of gene product greater than that expressed prior to manipulation of the microorganism or in a comparable microorganism which has not been manipulated. Genetic manipulation can include, but is not limited to, altering or modifying regulatory sequences or sites associated with expression of a particular gene (*e.g.*, by adding strong promoters, inducible promoters or multiple promoters or by removing regulatory sequences such that expression is constitutive), modifying the chromosomal location of a particular gene, altering nucleic acid sequences adjacent to a particular gene such as a ribosome binding site or transcription terminator, increasing the copy number of a particular gene, modifying proteins (*e.g.*, regulatory proteins, suppressors, enhancers, transcriptional activators and the like) involved in transcription of a particular gene and/or translation of a particular gene product, or any other conventional means of deregulating expression of a particular gene routine in the art (including but not limited to use of antisense nucleic acid molecules, for example, to block expression of repressor proteins).

In another embodiment, the microorganism can be physically or environmentally manipulated to overexpress a level of gene product greater than that expressed prior to manipulation of the microorganism or in a comparable microorganism which has not been manipulated. For example, a microorganism can be treated with or cultured in the presence of an agent known or suspected to increase transcription of a particular gene and/or translation of a particular gene product such that transcription and/or translation are enhanced or increased. Alternatively, a microorganism can be cultured at a temperature selected to increase transcription of a particular gene and/or translation of a particular gene product such that transcription and/or translation are enhanced or increased.

The term "deregulated" or "deregulation" includes the alteration or modification of at least one gene in a microorganism that encodes an enzyme in a biosynthetic pathway, such that the level or activity of the biosynthetic enzyme in the microorganism is altered or modified. Preferably, at least one gene that encodes an enzyme in a biosynthetic pathway is altered or modified such that the gene product is enhanced or increased. The phrase "deregulated pathway" can also include a biosynthetic pathway in

which more than one gene that encodes an enzyme in a biosynthetic pathway is altered or modified such that the level or activity of more than one biosynthetic enzyme is altered or modified. The ability to "deregulate" a pathway (*e.g.*, to simultaneously deregulate more than one gene in a given biosynthetic pathway) in a microorganism
5 arises from the particular phenomenon of microorganisms in which more than one enzyme (*e.g.*, two or three biosynthetic enzymes) are encoded by genes occurring adjacent to one another on a contiguous piece of genetic material termed an "operon".

The term "operon" includes a coordinated unit of gene expression that contains a promoter and possibly a regulatory element associated with one or more, preferably at
10 least two, structural genes (*e.g.*, genes encoding enzymes, for example, biosynthetic enzymes). Expression of the structural genes can be coordinately regulated, for example, by regulatory proteins binding to the regulatory element or by anti-termination of transcription. The structural genes can be transcribed to give a single mRNA that encodes all of the structural proteins. Due to the coordinated regulation of genes
15 included in an operon, alteration or modification of the single promoter and/or regulatory element can result in alteration or modification of each gene product encoded by the operon. Alteration or modification of the regulatory element can include, but is not limited to removing the endogenous promoter and/or regulatory element(s), adding strong promoters, inducible promoters or multiple promoters or removing regulatory
20 sequences such that expression of the gene products is modified, modifying the chromosomal location of the operon, altering nucleic acid sequences adjacent to the operon or within the operon such as a ribosome binding site, increasing the copy number of the operon, modifying proteins (*e.g.*, regulatory proteins, suppressors, enhancers, transcriptional activators and the like) involved in transcription of the operon and/or
25 translation of the gene products of the operon, or any other conventional means of deregulating expression of genes routine in the art (including but not limited to use of antisense nucleic acid molecules, for example, to block expression of repressor proteins). Deregulation can also involve altering the coding region of one or more genes to yield, for example, an enzyme that is feedback resistant or has a higher or lower
30 specific activity.

A particularly preferred "recombinant" microorganism of the present invention has been genetically engineered to overexpress a bacterially-derived gene or gene product. The term "bacterially-derived" or "derived-from", for example bacteria, includes a gene which is naturally found in bacteria or a gene product (*e.g.*, ketopantoate
35 hydroxymethyltransferase, ketopantoate reductase, pantothenate synthetase, aspartate- α -decarboxylate, acetohydroxyacid synthetase, acetohydroxyacid isomeroreductase or

dihydroxyacid dehydratase) which is encoded by a bacterial gene (e.g., encoded by *panB*, *panE*, *panC*, *panD*, *ilvB*, *ilvN*, *alsS*, *ilvC*, or *ilvD*).

The methodologies of the present invention feature recombinant microorganisms which overexpress at least one of ketopantoate hydroxymethyltransferase, ketopantoate reductase, pantothenate synthetase or aspartate- α -decarboxylase. A particularly preferred recombinant microorganism of the present invention has been genetically engineered to overexpress a *Bacillus* (e.g., *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus halodurans*, *Bacillus subtilis*, and *Bacillus pumilus*, etc.) biosynthetic enzyme (e.g., has been engineered to overexpress at least one of *B. subtilis* ketopantoate reductase (the *panE* gene product) (e.g., ketopantoate reductase having the amino acid sequence of SEQ ID NO:30 or encoded by the nucleic acid sequence of SEQ ID NO:29), *B. subtilis* ketopantoate hydroxymethyltransferase (the *panB* gene product) (e.g., ketopantoate hydroxymethyltransferase having the amino acid sequence of SEQ ID NO:24 or encoded by a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:23), *B. subtilis* pantothenate synthetase (the *panC* gene product) (e.g., pantothenate synthetase having the amino acid sequence of SEQ ID NO:26 or encoded by a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:25) and/or *B. subtilis* aspartate- α -decarboxylase (the *panD* gene product) (e.g., aspartate- α -decarboxylase having the amino acid sequence of SEQ ID NO:28 or encoded by a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:27).

In an exemplary embodiment, the invention features a microorganism (e.g., a KPAR-O microorganism) that has been transformed with a vector comprising a *panE* nucleic acid sequence (e.g., a *panE* nucleic acid sequence as set forth in SEQ ID NO:29). In another embodiment, the invention features a microorganism that has been transformed with a vector comprising a *panB* nucleic acid sequence (e.g., a *panB* nucleic acid sequence as set forth in SEQ ID NO:23), a vector comprising a *panC* nucleic acid sequence (e.g., a *panC* nucleic acid sequence as set forth in SEQ ID NO:25) or a vector comprising a *panD* nucleic acid sequence (e.g., a *panD* nucleic acid sequence as set forth in SEQ ID NO:27). In yet another embodiment, the invention features a microorganism having a deregulated *panBCD* operon (e.g., SEQ ID NO:59).

Other preferred "recombinant" microorganisms of the present invention have a deregulated isoleucine-valine (*ilv*) pathway. The phrase "microorganism having a deregulated isoleucine-valine (*ilv*) pathway" includes a microorganism having an alteration or modification in at least one gene encoding an enzyme of the isoleucine-valine (*ilv*) pathway or having an alteration or modification in an operon including more than one gene encoding an enzyme of the isoleucine-valine (*ilv*) pathway. A preferred "microorganism having a deregulated isoleucine-valine (*ilv*) pathway" has been

genetically engineered to overexpress a *Bacillus* (e.g., *B. subtilis*) *ilv* biosynthetic enzyme (e.g., has been engineered to overexpress at least one of acetohydroxyacid synthetase (the *ilvBN* gene products or the *alsS* gene product) (e.g., acetohydroxyacid synthetase having subunits having the amino acid sequences of SEQ ID NO:32 and SEQ ID NO:34 or encoded by nucleic acid molecules having the nucleotide sequence of SEQ ID NO:31 and SEQ ID NO:33 or the nucleotide sequence of SEQ ID NO:58 from nucleotides 1-2246 or acetohydroxyacid synthetase encoded by a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:86), acetohydroxyacid isomeroreductase (the *ilvC* gene product) (e.g., acetohydroxyacid isomeroreductase having the amino acid sequence of SEQ ID NO:36 or encoded by a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:35), dihydroxyacid dehydratase (the *ilvD* gene product) (e.g., dihydroxyacid dehydratase having the amino acid sequence of SEQ ID NO:38 or encoded by a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:37), and/or has been transformed with a vector comprising an *ilvBNC* nucleic acid sequence (SEQ ID NO:58, coding regions from nucleotides 1-1725, 1722-2246 and 2263-3291) and/or an *ilvD* nucleic acid sequence (SEQ ID NO:37).

In another preferred embodiment, a recombinant microorganism is designed or engineered such that a mutant CoaA and/or CoaX biosynthetic enzyme is expressed and at least one pantothenate biosynthetic enzyme and/or at least one isoleucine-valine biosynthetic enzyme is overexpressed or deregulated.

In another preferred embodiment, a microorganism of the present invention overexpresses or is mutated for a gene or biosynthetic enzyme (e.g., a CoA biosynthetic enzyme, pantothenate biosynthetic enzyme or isoleucine-valine biosynthetic enzyme) which is bacterially-derived. The term "bacterially-derived" or "derived-from", for example bacteria, includes a gene product (e.g., ketopantoate hydroxymethyltransferase, ketopantoate reductase, pantothenate synthetase, aspartate- α -decarboxylate, acetohydroxyacid synthetase, acetohydroxyacid isomeroreductase, dihydroxyacid dehydratase or pantothenate kinase) which is encoded by a bacterial gene (e.g., *panB*, *panE*, *panC*, *panD*, *ilvBN* (or *alsS*), *ilvC*, *ilvD*, or encoded by *coaA* or *coaX*).

Still other preferred recombinant microorganisms of the present invention are mutant microorganisms. As used herein, the term "mutant microorganism" includes a recombinant microorganism that has been genetically engineered to express a mutated gene or protein that is normally or naturally expressed by the microorganism.

Preferably, a mutant microorganism expresses a mutated gene or protein such that the microorganism exhibits an altered, modified or different phenotype (e.g., has been engineered to express a mutated CoaA biosynthetic enzyme, for example, pantothenate kinase). In one embodiment, a mutant microorganism is designed or engineered such

that it includes a mutant *coaX* gene, as defined herein. In another embodiment, a recombinant microorganism is designed or engineered such that it includes a mutant *coaA* gene, as defined herein. In another embodiment, a mutant microorganism is designed or engineered such that a *coaX* gene has been deleted (*i.e.*, the protein encoded by the *coaX* gene is not produced). In another embodiment, a mutant microorganism is designed or engineered such that a *coaA* gene has been deleted (*i.e.*, the protein encoded by the *coaA* gene is not produced). Preferably, a mutant microorganism has a mutant *coaX* gene or a mutant *coaA* gene, or has been engineered to have a *coaX* gene and/or *coaA* deleted, such that that the mutant microorganism encodes a “reduced pantothenate kinase activity”. In the context of a whole microorganism, a “reduced pantothenate kinase activity” can be determined by measuring or assaying for a decrease in an intermediate or product of the CoA biosynthetic pathway, for example, measuring or assaying for 4'-phosphopantothenate, 4'-phosphopantothenylcysteine, 4'-phosphopantetheine, dephosphocoenzyme A, Coenzyme A, apo-acyl carrier protein (apo-ACP) or holo-acyl carrier protein (ACP) in the microorganism (*e.g.*, in a lysate isolated or derived from the microorganism) or in the medium in which the microorganism is cultured (see *e.g.*, Figure 16). Alternatively, a “reduced pantothenate kinase activity” can be determined by measuring or assaying for decreased growth of the microorganism. Alternatively, a “reduced pantothenate kinase activity” can be determined by measuring or assaying for an increase in a panto-compound (*e.g.*, pantothenate) in the microorganism or surrounding media, as panto-compounds lie upstream of the CoA biosynthetic pathway, the first step of which is catalyzed by pantothenate kinase. The invention also features recombinant microorganisms that, in addition to having reduced pantothenate kinase activity (*e.g.*, expressing mutant *coaA* and/or mutant *coaX* genes) have a deregulated pantothenate biosynthesis pathway and/or a deregulated isoleucine-valine (*ilv*) biosynthetic pathway.

In one embodiment, a recombinant microorganism of the present invention is a Gram positive organism (*e.g.*, a microorganism which retains basic dye, for example, crystal violet, due to the presence of a Gram-positive wall surrounding the microorganism). In a preferred embodiment, the recombinant microorganism is a microorganism belonging to a genus selected from the group consisting of *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*. In a more preferred embodiment, the recombinant microorganism is of the genus *Bacillus*. In another preferred embodiment, the recombinant microorganism is selected from the group consisting of *Bacillus subtilis*, *Bacillus lentimorbus*, *Bacillus lentus*, *Bacillus firmus*, *Bacillus pantothenicus*, *Bacillus amyloliquefaciens*, *Bacillus cereus*, *Bacillus circulans*, *Bacillus coagulans*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*,

Bacillus thuringiensis, and other Group 1 *Bacillus* species, for example, as characterized by 16S rRNA type (Priest (1993) in *Bacillus subtilis and Other Gram-Positive Bacteria* eds. Sonenshein *et al.*, ASM, Washington, D.C., p. 6). In another preferred embodiment, the recombinant microorganism is *Bacillus brevis* or *Bacillus*
5 *stearothermophilus*. In another preferred embodiment, the recombinant microorganism is selected from the group consisting of *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus halodurans*, *Bacillus subtilis*, and *Bacillus pumilus*.

In another embodiment, the recombinant microorganism is a Gram negative (excludes basic dye) organism. In a preferred embodiment, the recombinant
10 microorganism is a microorganism belonging to a genus selected from the group consisting of *Salmonella*, *Escherichia*, *Klebsiella*, *Serratia*, and *Proteus*. In a more preferred embodiment, the recombinant microorganism is of the genus *Escherichia*. In an even more preferred embodiment, the recombinant microorganism is *Escherichia coli*. In another embodiment, the recombinant microorganism is *Saccharomyces* (e.g., *S.*
15 *cerevisiae*).

An important aspect of the present invention involves culturing the recombinant microorganisms described herein, such that a desired compound (e.g., a desired panto-compound) is produced. The term "culturing" includes maintaining and/or growing a living microorganism of the present invention (e.g., maintaining and/or growing a
20 culture or strain). In one embodiment, a microorganism of the invention is cultured in liquid media. In another embodiment, a microorganism of the invention is cultured in solid media or semi-solid media. In a preferred embodiment, a microorganism of the invention is cultured in media (e.g., a sterile, liquid media) comprising nutrients essential or beneficial to the maintenance and/or growth of the microorganism (e.g.,
25 carbon sources or carbon substrate, for example complex carbohydrates such as bean or grain meal, starches, sugars, sugar alcohols, hydrocarbons, oils, fats, fatty acids, organic acids and alcohols; nitrogen sources, for example, vegetable proteins, peptones, peptides and amino acids derived from grains, beans and tubers, proteins, peptides and amino acids derived from animal sources such as meat, milk and animal byproducts such as
30 peptones, meat extracts and casein hydrolysates; inorganic nitrogen sources such as urea, ammonium sulfate, ammonium chloride, ammonium nitrate and ammonium phosphate; phosphorus sources, for example, phosphoric acid, sodium and potassium salts thereof; trace elements, for example, magnesium, iron, manganese, calcium, copper, zinc, boron, molybdenum, and/or cobalt salts; as well as growth factors such as
35 amino acids, vitamins, growth promoters and the like).

Preferably, microorganisms of the present invention are cultured under controlled pH. The term "controlled pH" includes any pH which results in production of the desired product (e.g., a panto-compound). In one embodiment, microorganisms are cultured at a pH of about 7. In another embodiment, microorganisms are cultured at a pH of between 6.0 and 8.5. The desired pH may be maintained by any number of methods known to those skilled in the art.

Also preferably, microorganisms of the present invention are cultured under controlled aeration. The term "controlled aeration" includes sufficient aeration (e.g., oxygen) to result in production of the desired product (e.g., panto-compound). In one embodiment, aeration is controlled by regulating oxygen levels in the culture, for example, by regulating the amount of oxygen dissolved in culture media. Preferably, aeration of the culture is controlled by agitating the culture. Agitation may be provided by a propeller or similar mechanical agitation equipment, by revolving or shaking the growth vessel (e.g., fermentor) or by various pumping equipment. Aeration may be further controlled by the passage of sterile air or oxygen through the medium (e.g., through the fermentation mixture). Also preferably, microorganisms of the present invention are cultured without excess foaming (e.g., *via* addition of antifoaming agents).

Moreover, microorganisms of the present invention can be cultured under controlled temperatures. The term "controlled temperature" includes any temperature which results in production of the desired product (e.g., a panto-compound). In one embodiment, controlled temperatures include temperatures between 15°C and 95°C. In another embodiment, controlled temperatures include temperatures between 15°C and 70°C. Preferred temperatures are between 20°C and 55°C, more preferably between 30°C and 45°C or between 30°C and 50°C.

Microorganisms can be cultured (e.g., maintained and/or grown) in liquid media and preferably are cultured, either continuously or intermittently, by conventional culturing methods such as standing culture, test tube culture, shaking culture (e.g., rotary shaking culture, shake flask culture, etc.), aeration spinner culture, or fermentation. In a preferred embodiment, the microorganisms are cultured in shake flasks. In a more preferred embodiment, the microorganisms are cultured in a fermentor (e.g., a fermentation process). Fermentation processes of the present invention include, but are not limited to, batch, fed-batch and continuous methods of fermentation. The phrase "batch process" or "batch fermentation" refers to a closed system in which the composition of media, nutrients, supplemental additives and the like is set at the beginning of the fermentation and not subject to alteration during the fermentation, however, attempts may be made to control such factors as pH and oxygen concentration to prevent excess media acidification and/or microorganism death. The phrase "fed-

batch process" or "fed-batch" fermentation refers to a batch fermentation with the exception that one or more substrates or supplements are added (*e.g.*, added in increments or continuously) as the fermentation progresses. The phrase "continuous process" or "continuous fermentation" refers to a system in which a defined

5 fermentation media is added continuously to a fermentor and an equal amount of used or "conditioned" media is simultaneously removed, preferably for recovery of the desired product (*e.g.*, panto-compound). A variety of such processes have been developed and are well-known in the art.

The phrase "culturing under conditions such that a desired compound (*e.g.*, a
10 panto-compound, for example, pantothenate) is produced" includes maintaining and/or growing microorganisms under conditions (*e.g.*, temperature, pressure, pH, duration, etc.) appropriate or sufficient to obtain production of the desired compound or to obtain desired yields of the particular compound being produced. For example, culturing is continued for a time sufficient to produce the desired amount of a panto-compound (*e.g.*,
15 pantothenate, pantoate or β -alanine). Preferably, culturing is continued for a time sufficient to substantially reach maximal production of the panto-compound. In one embodiment, culturing is continued for about 12 to 24 hours. In another embodiment, culturing is continued for about 24 to 36 hours, 36 to 48 hours, 48 to 72 hours, 72 to 96 hours, 96 to 120 hours, 120 to 144 hours, or greater than 144 hours. In another
20 embodiment, culturing is continued for a time sufficient to reach production yields of panto-compound, for example, cells are cultured such that at least about 15 to 20 g/L of panto-compound are produced, at least about 20 to 25 g/L panto-compound are produced, at least about 25 to 30 g/L panto-compound are produced, at least about 30 to 35 g/L panto-compound are produced, at least about 35 to 40 g/L panto-compound are
25 produced (*e.g.*, at least about 37 g/L panto-compound) or at least about 40 to 50 g/L panto compound are produced. In yet another embodiment, microorganisms are cultured under conditions such that a preferred yield of panto-compound, for example, a yield within a range set forth above, is produced in about 24 hours, in about 36 hours, in about 48 hours, in about 72 hours, or in about 96 hours.

30 The methodology of the present invention can further include a step of recovering a desired compound (*e.g.*, a panto-compound). The term "recovering" a desired compound (*e.g.*, a panto-compound) includes extracting, harvesting, isolating or purifying the compound from culture media. Recovering the compound can be performed according to any conventional isolation or purification methodology known
35 in the art including, but not limited to, treatment with a conventional resin (*e.g.*, anion or cation exchange resin, non-ionic adsorption resin, etc.), treatment with a conventional adsorbent (*e.g.*, activated charcoal, silicic acid, silica gel, cellulose, alumina, etc.),

alteration of pH, solvent extraction (*e.g.*, with a conventional solvent such as an alcohol, ethyl acetate, hexane and the like), dialysis, filtration, concentration, crystallization, recrystallization, pH adjustment, lyophilization and the like. For example, a compound (*e.g.*, a panto-compound) can be recovered from culture media by first removing the
5 microorganisms from the culture. Media is then passed through or over a cation exchange resin to remove unwanted cations and then through or over an anion exchange resin to remove unwanted inorganic anions and organic acids having stronger acidities than the panto-compound of interest (*e.g.*, pantothenate). The resulting panto-compound (*e.g.*, pantothenate) can subsequently be converted to a pantothenate salt (*e.g.*, calcium
10 pantothenate) as described herein.

Preferably, a desired compound of the present invention is "extracted", "isolated" or "purified" such that the resulting preparation is substantially free of other components (*e.g.*, free of media components and/or fermentation byproducts). The language "substantially free of other components" includes preparations of desired
15 compound in which the compound is separated (*e.g.*, purified or partially purified) from media components or fermentation byproducts of the culture from which it is produced. In one embodiment, the preparation has greater than about 80% (by dry weight) of the desired compound (*e.g.*, less than about 20% of other media components or fermentation byproducts), more preferably greater than about 90% of the desired compound (*e.g.*, less
20 than about 10% of other media components or fermentation byproducts), still more preferably greater than about 95% of the desired compound (*e.g.*, less than about 5% of other media components or fermentation byproducts), and most preferably greater than about 98-99% desired compound (*e.g.*, less than about 1-2% other media components or fermentation byproducts). When the desired compound is a panto-compound that has
25 been derivatized to a salt (*e.g.* a pantothenate salt or pantoate salt), the panto-compound is preferably further free (*e.g.*, substantially free) of chemical contaminants associated with the formation of the salt. When the desired compound is a panto-compound that has been derivatized to an alcohol, the panto-compound is preferably further free (*e.g.*, substantially free) of chemical contaminants associated with the formation of the
30 alcohol.

In an alternative embodiment, the desired panto-compound is not purified from the microorganism, for example, when the microorganism is biologically non-hazardous (*e.g.*, safe). For example, the entire culture (or culture supernatant) can be used as a source of product (*e.g.*, crude product). In one embodiment, the culture (or culture
35 supernatant) supernatant is used without modification. In another embodiment, the culture (or culture supernatant) is concentrated. In yet another embodiment, the culture (or culture supernatant) is dried or lyophilized.

II. Panto-Compound Production Methodologies Featuring Ketopantoate Reductase-Overexpressing Microorganisms

One aspect of the invention features methods of producing a panto-compounds that involve culturing a ketopantoate reductase-overexpressing (KPAR-O) microorganism under conditions such that the panto-compound is produced. The term “ketopantoate reductase-overexpressing (KPAR-O) microorganism” includes a microorganism which has been manipulated such that ketopantoate reductase is overexpressed (e.g., a *B. subtilis* ketopantoate reductase protein having the amino acid sequence of SEQ ID NO:30) and/or has been transformed with a vector comprising a *panE1* nucleic acid sequence (e.g., a *B. subtilis panE1* nucleic acid sequence as set forth in SEQ ID NO:29). In one embodiment, the panto-compound is pantothenate. In another embodiment, the panto-compound is pantoate. In another embodiment, the ketopantoate reductase is bacterial-derived. In another embodiment, the ketopantoate reductase is derived from *Bacillus* (e.g., is derived from *Bacillus subtilis*). In yet another embodiment, the KPAR-O microorganism is Gram positive. In yet another embodiment, the KPAR-O microorganism is a microorganism belonging to a genus selected from the group consisting of *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*. In a preferred embodiment, the KPAR-O microorganism is of the genus *Bacillus*. In a more preferred embodiment, the KPAR-O microorganism is selected from the group consisting of *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus halodurans*, *Bacillus subtilis* and *Bacillus pumilus*. In a particularly preferred embodiment, the KPAR-O microorganism is *Bacillus subtilis*.

In still other embodiments, the KPAR-O microorganism further overexpresses at least one pantothenate biosynthetic enzyme in addition to ketopantoate reductase. In an exemplary embodiment, the KPAR-O microorganism further overexpresses at least one of ketopantoate hydroxymethyltransferase, pantothenate synthetase and aspartate- α -decarboxylase. Also featured are methods of producing panto-compounds, for example, methods that involve culturing a KPAR-O microorganism, which further include the step of recovering the panto-compound.

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III. Methods of Producing Panto-Compounds Independent of Precursor Feed Requirements

Depending on the biosynthetic enzyme or combination of biosynthetic enzymes manipulated, it may be desirable or necessary to provide (e.g., feed) microorganisms of the present invention at least one pantothenate biosynthetic precursor such that pantothenate or other desired panto-compounds are produced. The term “pantothenate biosynthetic precursor” or “precursor” includes an agent or compound which, when

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provided to, brought into contact with, or included in the culture medium of a microorganism, serves to enhance or increase pantothenate biosynthesis. In one embodiment, the pantothenate biosynthetic precursor or precursor is aspartate. In another embodiment, the pantothenate biosynthetic precursor or precursor is β -alanine.

- 5 The amount of aspartate or β -alanine added is preferably an amount that results in a concentration in the culture medium sufficient to enhance productivity of the microorganism (*e.g.*, a concentration sufficient to enhance production of a panto-compound, for example, β -alanine, ketopantoate, pantoate or pantothenate).

Pantothenate biosynthetic precursors of the present invention can be added in the form
10 of a concentrated solution or suspension (*e.g.*, in a suitable solvent such as water or buffer) or in the form of a solid (*e.g.*, in the form of a powder). Moreover, pantothenate biosynthetic precursors of the present invention can be added as a single aliquot, continuously or intermittently over a given period of time.

In yet another embodiment, the pantothenate biosynthetic precursor is valine, see
15 *e.g.*, Example III. In yet another embodiment, the pantothenate biosynthetic precursor is α -ketoisovalerate. Preferably, valine or α -ketoisovalerate is added in an amount that results in a concentration in the medium sufficient for production of the desired product (*e.g.*, panto-compound) to occur. Pantothenate biosynthetic precursors are also referred to herein as "supplemental pantothenate biosynthetic substrates".

20 Providing pantothenate biosynthetic precursors in the pantothenate biosynthetic methodologies of the present invention, can be associated with high costs, for example, when the methodologies are used to produce high yields of panto-compounds. Accordingly, preferred methodologies of the present invention feature microorganisms having at least one biosynthetic enzyme or combination of biosynthetic enzymes (*e.g.*, at
25 least one pantothenate biosynthetic enzyme and/or valine-isoleucine biosynthetic enzyme) manipulated such that pantothenate or other desired panto-compounds are produced in a manner independent of precursor feed. The phrase "a manner independent of precursor feed", for example, when referring to a method for producing a desired compound (*e.g.*, a panto-compound), includes an approach to or a mode of
30 producing the desired compound that does not depend or rely on precursors being provided (*e.g.*, fed) to the microorganism being utilized to produce the desired compound. For example, microorganisms featured in the methodologies of the present invention can be used to produce panto-compounds in a manner requiring no feeding of the precursors aspartate, β -alanine, valine and/or α -KIV.

35 Alternative preferred methodologies of the present invention feature microorganisms having at least one biosynthetic enzyme or combination of biosynthetic enzymes manipulated such that pantothenate or other desired panto-compounds are

produced in a manner substantially independent of precursor feed. The phrase "a manner substantially independent of precursor feed" includes an approach to or a method of producing the desired compound that depends or relies to a lesser extent on precursors being provided (*e.g.*, fed) to the microorganism being utilized. For example, microorganisms featured in the methodologies of the present invention can be used to produce panto-compounds in a manner requiring feeding of substantially reduced amounts of the precursors aspartate, β -alanine, valine and/or α -KIV. In one embodiment, the invention features methods of producing panto-compounds (*e.g.*, pantothenate) in a manner that requires feeding of less than 5%-10% of the amount of precursor required by a control microorganism (*e.g.*, a microorganism that is dependent, for example is wholly dependent, on precursor feed to efficiently produce the desired compound). In another embodiment, the invention features methods of producing panto-compounds in a manner that requires feeding of less than 15-20% of the amount of precursor required by a control microorganism. In another embodiment, the invention features methods of producing panto-compounds in a manner that requires feeding of less than 25-30%, 35-40%, 45-50% or 55-60% of the amount of precursor required by a control microorganism. As described in Examples I-III herein, particular microorganisms featured in the methodologies of the present invention require, for example, 5 g/L of aspartate, β -alanine, valine or α -KIV (*e.g.*, in test tube or in shake flask cultures). Accordingly, in a preferred embodiment, the present invention features methods of producing panto-compounds (*e.g.*, pantothenate) in a manner requiring feeding of less than 0.25 g/L, 0.5 g/L, 0.75 g/L, 1 g/L, 1.25 g/L, 1.5 g/L, 1.75 g/L, 2 g/L, 2.25 g/L, 2.5 g/L, 2.75 g/L or 3 g/L.

Preferred methods of producing desired compounds (*e.g.*, panto-compounds) in a manner independent of precursor feed or alternatively, in a manner substantially independent of precursor feed, involve culturing microorganisms which have been manipulated (*e.g.*, designed or engineered, for example, genetically engineered) such that expression of at least one pantothenate biosynthetic enzyme, and/or at least one isoleucine-valine biosynthetic enzyme, is modified. For example, in one embodiment, a microorganism is manipulated (*e.g.*, designed or engineered) such that the production of at least one pantothenate biosynthetic enzyme, and/or at least one isoleucine/valine biosynthetic enzyme is deregulated. In a preferred embodiment, a microorganism is manipulated (*e.g.*, designed or engineered) such that it has a deregulated biosynthetic pathway, for example, a deregulated pantothenate biosynthesis pathway and/or a deregulated isoleucine-valine biosynthetic pathway, as defined herein. In another preferred embodiment, a microorganism is manipulated (*e.g.*, designed or engineered)

such that at least one pantothenate biosynthetic enzyme, and/or at least one isoleucine-valine biosynthetic enzyme is overexpressed.

Preferred methods of producing desired compounds (*e.g.*, panto-compounds) in a manner independent of precursor feed or alternatively, in a manner substantially independent of precursor feed, are as follows. In one embodiment, the invention features a method of producing pantothenate in a manner independent of precursor feed comprising culturing an aspartate- α -decarboxylase-overexpressing (A α D-O) microorganism having a deregulated isoleucine-valine (*ilv*) pathway under conditions such that pantothenate is produced. In another embodiment, the invention features a method of producing pantothenate in a manner independent of precursor feed comprising culturing an aspartate- α -decarboxylase-overexpressing (A α D-O) microorganism having a deregulated pantothenate (*pan*) pathway and a deregulated isoleucine-valine (*ilv*) pathway, under conditions such that pantothenate is produced. In another embodiment, the invention features a method of producing pantothenate in a manner independent of aspartate or β -alanine feed comprising culturing an aspartate- α -decarboxylase-overexpressing (A α D-O) microorganism under conditions such that pantothenate is produced. In yet another embodiment, the invention features a method of producing pantothenate in a manner independent of valine or α -ketoisovalerate feed comprising culturing a microorganism having a deregulated isoleucine-valine (*ilv*) biosynthetic pathway under conditions such that pantothenate is produced.

The term "aspartate- α -decarboxylase-overexpressing (A α D-O) microorganism" includes a microorganism which has been manipulated such that aspartate- α -decarboxylase is overexpressed. A preferred "aspartate- α -decarboxylase-overexpressing (A α D-O) microorganism" has been transformed with a vector comprising a *B. subtilis* *panD* nucleic acid sequence (*e.g.*, a *panD* nucleic acid sequence that encodes an aspartate- α -decarboxylase protein having the amino acid sequence of SEQ ID NO:28, for example, a *panD* nucleic acid sequence as set forth in SEQ ID NO:27).

The phrase "microorganism having a deregulated isoleucine-valine (*ilv*) pathway" includes a microorganism having an alteration or modification in at least one gene encoding an enzyme of the isoleucine-valine (*ilv*) pathway or having an alteration or modification in an operon including more than one gene encoding an enzyme of the isoleucine-valine (*ilv*) pathway. A preferred "microorganism having a deregulated isoleucine-valine (*ilv*) pathway" overexpresses acetohydroxyacid synthetase (*e.g.*, acetohydroxyacid synthetase having subunits having the amino acid sequences of SEQ ID NO:32 and SEQ ID NO:34 or acetohydroxyacid synthetase having the amino acid sequence of SEQ ID NO:87), acetohydroxyacid isomeroreductase (having the amino acid sequence of SEQ ID NO:36), or dihydroxyacid dehydratase (having the amino acid

sequence of SEQ ID NO:38) and/or has been transformed with a vector comprising *ilvB*, *ilvN*, *ilvC*, *ilvBN*, *ilvBNC* or *alsS* nucleic acid sequences (SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, nucleotides 1-2246 of SEQ ID NO:58, SEQ ID NO:58 having coding regions from nucleotides 1-1725, 1722-2246 and 2263-3291, or SEQ ID NO:86, respectively) and/or an *ilvD* nucleic acid sequence (SEQ ID NO:37).

IV. High Yield Production Methodologies

A particularly preferred embodiment of the present invention is a high yield production method for producing pantothenate comprising culturing a manipulated microorganism under conditions such that pantothenate is produced at a significantly high yield. The phrase "high yield production method", for example, a high yield production method for producing a desired compound (e.g., for producing a panto-compound) includes a method that results in production of the desired compound at a level which is elevated or above what is usual for comparable production methods.

Preferably, a high yield production method results in production of the desired compound at a significantly high yield. The phrase "significantly high yield" includes a level of production or yield which is sufficiently elevated or above what is usual for comparable production methods, for example, which is elevated to a level sufficient for commercial production of the desired product (e.g., production of the product at a commercially feasible cost). In one embodiment, the invention features a high yield production method of producing pantothenate that includes culturing a manipulated microorganism under conditions such that pantothenate is produced at a level greater than 2 g/L. In another embodiment, the invention features a high yield production method of producing pantothenate that includes culturing a manipulated microorganism under conditions such that pantothenate is produced at a level greater than 10 g/L. In another embodiment, the invention features a high yield production method of producing pantothenate that includes culturing a manipulated microorganism under conditions such that pantothenate is produced at a level greater than 20 g/L. In yet another embodiment, the invention features a high yield production method of producing pantothenate that includes culturing a manipulated microorganism under conditions such that pantothenate is produced at a level greater than 30 g/L. In yet another embodiment, the invention features a high yield production method of producing pantothenate that includes culturing a manipulated microorganism under conditions such that pantothenate is produced at a level greater than 40 g/L.

The invention further features a high yield production method for producing a desired compound (e.g., for producing a panto-compound) that involves culturing a manipulated microorganism under conditions such that a sufficiently elevated level of

compound is produced within a commercially desirable period of time. In an exemplary embodiment, the invention features a high yield production method of producing pantothenate that includes culturing a manipulated microorganism under conditions such that pantothenate is produced at a level greater than 15-20 g/L in 36 hours. In another embodiment, the invention features a high yield production method of producing pantothenate that includes culturing a manipulated microorganism under conditions such that pantothenate is produced at a level greater than 25-30 g/L in 48 hours. In another embodiment, the invention features a high yield production method of producing pantothenate that includes culturing a manipulated microorganism under conditions such that pantothenate is produced at a level greater than 35-40 g/L in 72 hours, for example, greater than 37 g/L in 72 hours. In another embodiment, the invention features a high yield production method of producing pantothenate that includes culturing a manipulated microorganism under conditions such that pantothenate is produced at a level greater than 30-40 g/L in 60 hours, for example, greater than 30, 35 or 40 g/L in 60 hours. Values and ranges included and/or intermediate within the ranges set forth herein are also intended to be within the scope of the present invention. For example, pantothenate production at levels of at least 31, 32, 33, 34, 35, 36, 37, 38 and 39 g/L in 60 hours are intended to be included within the range of 30-40 g/L in 60 hours. In another example, ranges of 30-35 g/L or 35-40 g/L are intended to be included within the range of 30-40 g/L in 60 hours. Moreover, the skilled artisan will appreciate that culturing a manipulated microorganism to achieve a production level of, for example, "30-40 g/L in 60 hours" includes culturing the microorganism for additional time periods (e.g., time periods longer than 60 hours), optionally resulting in even higher yields of pantothenate being produced.

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V. Panto-Compound Production Methodologies Featuring Pantothenate Kinase Mutant Microorganisms

The present invention relates to methods of producing pantothenate using microorganisms engineered to produce high yields of pantothenate as well as other panto-compounds. Cells overproducing pantothenate result in high intracellular pantothenate levels that could overcome the feedback inhibition of pantothenate kinase by CoA, leading to overproduction of CoA. Besides consuming pantothenate, increased synthesis of CoA may cause increased feedback inhibition of the PanB, PanD, PanE or PanC reaction, thereby limiting pantothenate production. Accordingly, a reduction in pantothenate kinase activity may lead to a decrease in CoA levels with resulting increases in PanB, PanD, PanE or PanC activity and pantothenate production.

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Thus, certain methodologies of the present invention are based, at least in part, on the identification and characterization of the *B. subtilis coaA* gene and the demonstration that the gene is neither essential for *B. subtilis* growth (*i.e.*, deletion of the *coaA* gene from the chromosome of *B. subtilis* is not a lethal event) nor for pantothenate kinase activity in *B. subtilis*. A second pantothenate kinase-encoding gene has been identified and characterized in *B. subtilis*, and is termed "*coaX*". This gene complements an *E. coli* mutant that contains a temperature sensitive pantothenate kinase and is not related by homology to any previously known pantothenate kinase gene.

In one aspect, the methodologies of the invention feature recombinant microorganisms that include the *coaX* gene or that include a mutant *coaX* gene, having reduced pantothenate kinase activity. In one embodiment, the methodologies feature such recombinant microorganisms further having a deregulated pantothenate biosynthetic pathway. In another embodiment, the methodologies feature such recombinant microorganisms further having a deregulated isoleucine-valine (*ilv*) pathway. In a preferred embodiment, the microorganisms belong to the genus *Bacillus* (*e.g.*, *B. subtilis*).

The methodologies of the invention also feature recombinant microorganisms (*e.g.*, microorganisms belong to the genus *Bacillus*, for example, *B. subtilis*) that include the *coaA* gene or that include a mutant *coaA* gene, optionally including a *coaX* gene or mutant thereof, having reduced pantothenate kinase activity. In one embodiment, the methodologies feature such recombinant microorganisms further having a deregulated pantothenate biosynthetic pathway or having a deregulated isoleucine-valine (*ilv*) pathway. Also featured are vectors that include isolated *coaX* or *coaA* genes as well as mutant *coaX* and/or *coaA* genes. Isolated nucleic acid molecules that include isolated *coaX* genes or mutant *coaX* genes are features in addition to isolated CoaX proteins and mutant CoaX proteins.

The above-described nucleic acid molecules (*e.g.*, genes), proteins, vectors, and recombinant microorganisms (*e.g.*, mutant microorganisms), are particularly suited for use in methods of producing panto-compounds and/or methods of enhancing panto-compound production. In one embodiment, the invention features a method for producing a panto-compound (*e.g.*, pantothenate) that includes culturing a pantothenate kinase mutant (*e.g.*, a recombinant microorganism that misexpresses, *e.g.*, is mutated for, pantothenate kinase, as defined herein) under conditions such that panto-compound is produced. In another embodiment, the invention features a method for enhancing production of a panto-compound (*e.g.*, pantothenate) that includes culturing a pantothenate kinase mutant (*e.g.*, a recombinant microorganism that misexpresses, *e.g.*, is mutated for, pantothenate kinase, as defined herein) under conditions such that

production of the panto-compound is produced. As used herein, the term "enhancing" (for example, in the context of the phrase "enhancing production") includes increasing the level or rate of production of panto-compound (e.g., pantothenate) as compared to the level or rate of production in a non-mutant microorganism (e.g., a microorganism having a normal pantothenate kinase gene(s) and/or having normal pantothenate production rates and/or levels.

Preferably, the level of panto-compound produced in methodologies featuring the pantothenate kinase mutants of the present invention is increased by at least 5% as compared to the level produced by a non-mutant (e.g., a recombinant microorganism expressing non-mutated pantothenate kinase). Even more preferably, the level of panto-compound is increased 10% as compared to methodologies featuring non-mutants. Even more preferably, panto-compound levels (e.g., pantothenate levels) are increased 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, are increased 2-fold, 5-fold, 10-fold, 50-fold, 100-fold or more as compared to methodologies featuring non-mutants.

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VI. Additional Mutations Resulting in Enhanced Panto-Compound Production

The methodologies of the present invention further can include, for example in addition to overexpressing or deregulating a pantothenate biosynthetic enzyme and/or an isoleucine-valine biosynthetic enzyme, or in addition to mutating a pantothenate-kinase encoding gene, deleting or mutating an enzyme that catalyzes the conversion of key pantothenate biosynthesis substrates or precursors to unwanted or undesirable products. For example, mutating the *ilvE* gene (Kuramitsu *et al.* (1985) *J. Biochem.* 97:993-999) or a homologue thereof (SEQ ID NO:62 or SEQ ID NO:64), thereby limiting the conversion of α -ketoisovalerate to valine, in addition to mutating a pantothenate kinase encoding enzyme, is predicted to result in even further enhanced or increased production of panto-compound. Alternatively, mutating the *ansB* gene (Sun and Seflow (1991) *J. Bacteriol.* 173:3831-3845) or a homologue thereof (SEQ ID NO:66), thereby limiting the degradation of aspartate, in addition to mutating a pantothenate kinase encoding enzyme, is predicted to result in even further enhanced or increased production of panto-compound. Alternatively, mutating the *alsD* gene (Renna *et al.* (1993) *J. Bacteriol.* 175:3863-3875) or a homologue thereof (SEQ ID NO:68), thereby limiting the conversion of acetolactate to acetoin, in addition to mutating a pantothenate kinase encoding enzyme, is predicted to result in even further enhanced or increased production of panto-compound. Alternatively, mutating the *avtA* gene encoding alanine-valine transaminase or a homologue thereof, thereby limiting the conversion of α -ketoisovalerate to valine, in addition to mutating a pantothenate kinase encoding

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enzyme, is predicted to result in even further enhanced or increased production of panto-compound. Mutating the *avtA* gene can include mutating, for example, an *avtA* gene having the nucleotide sequence of SEQ ID NO:70 (e.g., the *E. coli avtA* gene), or a structural homolog thereof (e.g., a homologue encoding a protein having 30-40%, 40-50%, 50-60%, 60-70%, 70-80%, 80-90%, 90-95% or more identity with the amino acid sequence of SEQ ID NO:71) or a functional homologue (e.g., a gene encoding a structurally unrelated protein having alanine-valine transaminase activity. Such mutations can be accomplished using the methodologies as exemplified in the Examples (e.g., Examples XIII, XV, XVI and XVII).

10 Accordingly, in one embodiment, the invention features a method of producing a panto-compound which includes culturing a microorganism having a mutant pantothenate kinase-encoding gene and which further has a deletion or mutation in an *avtA*, *ilvE*, *ansB*, and/or *alsD* gene, or homologue thereof. In another embodiment, the invention features a method of producing a panto-compound which includes culturing a
15 microorganism having a mutant pantothenate-kinase encoding gene and a deregulated pantothenate biosynthetic pathway enzyme and which further has a deletion or mutation in an *avtA*, *ilvE*, *ansB*, and/or *alsD* gene, or homologue thereof. In another embodiment, the invention features a method of producing a panto-compound which includes culturing a microorganism having a mutant pantothenate-kinase encoding gene and a
20 deregulated isoleucine-valine biosynthetic pathway enzyme and which further has a deletion or mutation in an *avtA*, *ilvE*, *ansB*, and/or *alsD* gene, or homologue thereof.

Mutating the *alsD* gene can be particularly useful when accomplished in conjunction with overexpression or deregulation of the *alsS* gene, for example, to prevent carbon (e.g., acetolactate) from being drawn away from the precursor pool
25 utilized for α -KIV production. Accordingly, to maximize the contribution of the *als* locus to panto-compound production, it is desirable to disrupt the *alsD* gene in addition to overexpressing the *alsS* gene. To disrupt the *alsD* gene, appropriate fragments of the *als* operon, flanking the *alsD* gene, are amplified by PCR and cloned to provide homology for creating the disruptions. A drug resistance gene, such as the *cat* gene, is
30 cloned between the flanking DNA fragments in place of the *alsD* gene, and the linearized DNA is transformed into a pantothenate production strain such as PA824, selecting for drug-resistance. To overexpress *alsS*, the *alsS* coding sequence (e.g., an *alsS* coding sequence that has been engineered by PCR for expression) is cloned into an expression vector. Vectors which express *alsS* (or alternatively, vectors which express
35 *alsS* plus *ilvC*) are introduced into panto-compound production strains (e.g., the pantothenate producing strain PA824).

The methodologies of the present invention further can include, for example in addition to overexpressing or deregulating a pantothenate biosynthetic enzyme and/or an isoleucine-valine biosynthetic enzyme, or in addition to mutating a pantothenate-kinase encoding gene, deleting or mutating an enzyme that catalyzes the conversion of desired panto-compounds to unwanted or undesirable downstream products.

VII. Isolated Nucleic Acid Molecules and Genes

Another aspect of the present invention features isolated nucleic acid molecules that encode *Bacillus* proteins (e.g., *B. subtilis* proteins), for example, *Bacillus* pantothenate biosynthetic enzymes (e.g., *B. subtilis* pantothenate biosynthetic enzymes) or *Bacillus* valine-isoleucine biosynthetic enzymes (e.g., *B. subtilis* valine-isoleucine biosynthetic enzymes). Also featured are isolated *coaX* and/or *coaA* nucleic acid molecules (e.g., isolated *coaX* and/or *coaA* genes) as well as isolated nucleic acid molecules that include such *coaX* and/or *coaA* nucleic acid molecules or genes.

The term "nucleic acid molecule" includes DNA molecules (e.g., linear, circular, cDNA or chromosomal DNA) and RNA molecules (e.g., tRNA, rRNA, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. The term "isolated" nucleic acid molecule includes a nucleic acid molecule which is free of sequences which naturally flank the nucleic acid molecule (i.e., sequences located at the 5' and 3' ends of the nucleic acid molecule) in the chromosomal DNA of the organism from which the nucleic acid is derived. In various embodiments, an isolated nucleic acid molecule can contain less than about 10 kb, 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb, 0.1 kb, 50 bp, 25 bp or 10 bp of nucleotide sequences which naturally flank the nucleic acid molecule in chromosomal DNA of the microorganism from which the nucleic acid molecule is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular materials when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized.

The term "gene", as used herein, includes a nucleic acid molecule (e.g., a DNA molecule or segment thereof), for example, a protein or RNA-encoding nucleic acid molecule, that in an organism, is separated from another gene or other genes, by intergenic DNA (i.e., intervening or spacer DNA which naturally flanks the gene and/or separates genes in the chromosomal DNA of the organism). A gene may direct synthesis of an enzyme or other protein molecule (e.g., may comprise coding sequences, for example, a contiguous open reading frame (ORF) which encodes a protein) or may itself be functional in the organism. A gene in an organism, may be clustered in an

operon, as defined herein, said operon being separated from other genes and/or operons by the intergenic DNA. Individual genes contained within an operon may overlap without intergenic DNA between said individual genes. An "isolated gene", as used herein, includes a gene which is essentially free of sequences which naturally flank the gene in the chromosomal DNA of the organism from which the gene is derived (*i.e.*, is free of adjacent coding sequences which encode a second or distinct protein or RNA molecule, adjacent structural sequences or the like) and optionally includes 5' and 3' regulatory sequences, for example promoter sequences and/or terminator sequences. In one embodiment, an isolated gene includes predominantly coding sequences for a protein (*e.g.*, sequences which encode *Bacillus* proteins). In another embodiment, an isolated gene includes coding sequences for a protein (*e.g.*, for a *Bacillus* protein) and adjacent 5' and/or 3' regulatory sequences from the chromosomal DNA of the organism from which the gene is derived (*e.g.*, adjacent 5' and/or 3' *Bacillus* regulatory sequences). Preferably, an isolated gene contains less than about 10 kb, 5 kb, 2 kb, 1 kb, 0.5 kb, 0.2 kb, 0.1 kb, 50 bp, 25 bp or 10 bp of nucleotide sequences which naturally flank the gene in the chromosomal DNA of the organism from which the gene is derived.

In one aspect, the present invention features isolated *panB* nucleic acid sequences or genes, isolated *panC* nucleic acid sequences or genes, isolated *panD* nucleic acid sequences or genes, isolated *panE* nucleic acid sequences or genes, isolated *ilvB*, *ilvN*, *ilvBN* nucleic acid sequences or genes, isolated *alsS* nucleic acid sequences or genes, isolated *ilvC* nucleic acid sequences or genes and/or isolated *ilvD* nucleic acid sequences or genes.

In a preferred embodiment, the nucleic acid or gene is derived from *Bacillus* (*e.g.*, is *Bacillus*-derived). The term "derived from *Bacillus*" or "*Bacillus*-derived" includes a nucleic acid or gene which is naturally found in microorganisms of the genus *Bacillus*. Preferably, the nucleic acid or gene is derived from a microorganism selected from the group consisting of *Bacillus subtilis*, *Bacillus lentimorbus*, *Bacillus lentus*, *Bacillus firmus*, *Bacillus pantothenicus*, *Bacillus amyloliquefaciens*, *Bacillus cereus*, *Bacillus circulans*, *Bacillus coagulans*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus thuringiensis*, and other Group 1 *Bacillus* species, for example, as characterized by 16S rRNA type (Priest, *supra*). In another preferred embodiment, the nucleic acid or gene is derived from *Bacillus brevis* or *Bacillus stearothermophilus*. In another preferred embodiment, the nucleic acid molecules and/or genes of the present invention are derived from a microorganism selected from the group consisting of *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus halodurans*, *Bacillus subtilis*, and *Bacillus pumilus*. In a particularly preferred

embodiment, the nucleic acid or gene is derived from *Bacillus subtilis* (e.g., is *Bacillus subtilis*-derived). The term "derived from *Bacillus subtilis*" or "*Bacillus subtilis*-derived" includes a nucleic acid or gene which is naturally found in *Bacillus subtilis*. In yet another preferred embodiment, the nucleic acid or gene is a *Bacillus* gene
5 homologue (e.g., is derived from a species distinct from *Bacillus* but having significant homology to a *Bacillus* gene of the present invention, for example, a *Bacillus pan* gene or *Bacillus ilv* gene).

Included within the scope of the present invention are bacterial-derived nucleic acid molecules or genes and/or *Bacillus*-derived nucleic acid molecules or genes (e.g.,
10 *B. subtilis*-derived nucleic acid molecules or genes), for example, the genes identified by the present inventors, for example, *Bacillus* or *B. subtilis coaX* genes, *coaA* genes, *pan* genes and/or *ilv* genes. Further included within the scope of the present invention are bacterial-derived nucleic acid molecules or genes and/or *Bacillus*-derived nucleic acid molecules or genes (e.g., *B. subtilis*-derived nucleic acid molecules or genes) (e.g., *B.*
15 *subtilis* nucleic acid molecules or genes) which differ from naturally-occurring bacterial and/or *Bacillus* nucleic acid molecules or genes (e.g., *B. subtilis* nucleic acid molecules or genes), for example, nucleic acid molecules or genes which have nucleic acids that are substituted, inserted or deleted, but which encode proteins substantially similar to the naturally-occurring gene products of the present invention. In one embodiment, an
20 isolated nucleic acid molecule comprises at least one of the nucleotide sequences set forth as SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO 31, SEQ ID NO:33, SEQ ID NO:86, SEQ ID NO:35 or SEQ ID NO:37. In another preferred embodiment, an isolated nucleic acid molecule comprises at least two, three or four of the nucleotide sequences set forth as SEQ ID NO:23, SEQ ID NO:25, SEQ ID
25 NO:27, SEQ ID NO:29, SEQ ID NO 31, SEQ ID NO:33, SEQ ID NO:88, SEQ ID NO:35 or SEQ ID NO:37. For example, a preferred isolated nucleic acid molecule of the present invention can include the nucleotide sequences of SEQ ID NO:23, SEQ ID NO:25 and SEQ ID NO:27, preferably linked such that the proteins encoded by the nucleotide sequences of SEQ ID NO:23, SEQ ID NO:25 and SEQ ID NO:27 are each
30 produced when the isolated nucleic acid molecule is expressed in a microorganism (e.g., SEQ ID NO:59). In another example, a preferred isolated nucleic acid molecule of the present invention can include the nucleotide sequences of SEQ ID NO:31 and SEQ ID NO:33, preferably linked such that the proteins encoded by the nucleotide sequences of SEQ ID NO:31 and SEQ ID NO:33 are each produced when the isolated nucleic acid
35 molecule is expressed in a microorganism (e.g., nucleotides 1-2246 of SEQ ID NO:58). In another example, a preferred isolated nucleic acid molecule of the present invention can include the nucleotide sequence of SEQ ID NO:86. In another example, a preferred

isolated nucleic acid molecule of the present invention can include the nucleotide sequences of SEQ ID NO:31, SEQ ID NO:33 and SEQ ID NO:35, preferably linked such that the proteins encoded by the nucleotide sequences of SEQ ID NO:31, SEQ ID NO:33 and SEQ ID NO:35 are each produced when the isolated nucleic acid molecule is expressed in a microorganism (e.g., SEQ ID NO:58).

In another embodiment, an isolated nucleic acid molecule of the present invention comprises a nucleotide sequence which is at least about 60-65%, preferably at least about 70-75%, more preferable at least about 80-85%, and even more preferably at least about 90-95% or more identical to a nucleotide sequence set forth as SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO 31, SEQ ID NO:33, SEQ ID NO:88, SEQ ID NO:35 or SEQ ID NO:37. In another embodiment, an isolated nucleic acid molecule hybridizes under stringent conditions to a nucleic acid molecule having a nucleotide sequence set forth as SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO 31, SEQ ID NO:33, SEQ ID NO:88, SEQ ID NO:35 or SEQ ID NO:37. Such stringent conditions are known to those skilled in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent (e.g. high stringency) hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO 31, SEQ ID NO:33, SEQ ID NO:88, SEQ ID NO:35 or SEQ ID NO:37 corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature.

A nucleic acid molecule of the present invention (e.g., a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO 31, SEQ ID NO:33, SEQ ID NO:88, SEQ ID NO:35 or SEQ ID NO:37 can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, nucleic acid molecules can be isolated using standard hybridization and cloning techniques (e.g., as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989) or can be isolated by the polymerase chain reaction using synthetic oligonucleotide primers designed based upon the sequence of SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO 31, SEQ ID NO:33, SEQ ID NO:88, SEQ ID NO:35 or SEQ ID NO:37. A nucleic acid of the invention can be

amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of the nucleotide
5 sequence shown in SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO 31, SEQ ID NO:33, SEQ ID NO:88, SEQ ID NO:35.

Additional *panC* nucleic acid sequences include those that comprise the nucleotide sequence of SEQ ID NO:25, encode a homologue of the polypeptide having the amino acid sequence set forth in SEQ ID NO:26 (e.g., encode a polypeptide having
10 at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or more identity to the polypeptide having the amino acid sequence as set forth in SEQ ID NO:26 and a substantially identical activity as said polypeptide), hybridize under stringent conditions to all or a portion of a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:25 or to all or a portion of a nucleic acid molecule that encodes a polypeptide having the
15 amino acid sequence of SEQ ID NO:26, or are complementary to a *panC* nucleotide sequence as set forth herein.

Additional *panD* nucleic acid sequences include those that comprise the nucleotide sequence of SEQ ID NO:27, encode a homologue of the polypeptide having the amino acid sequence set forth in SEQ ID NO:28 (e.g., encode a polypeptide having
20 at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or more identity to the polypeptide having the amino acid sequence as set forth in SEQ ID NO:28 and a substantially identical activity as said polypeptide), hybridize under stringent conditions to all or a portion of a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:27 or to all or a portion of a nucleic acid molecule that encodes a polypeptide having the
25 amino acid sequence of SEQ ID NO:28, or are complementary to a *panD* nucleotide sequence as set forth herein.

Additional *panE* nucleic acid sequences include those that comprise the nucleotide sequence of SEQ ID NO:29, encode a homologue of the polypeptide having the amino acid sequence set forth in SEQ ID NO:30 (e.g., encode a polypeptide having
30 at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or more identity to the polypeptide having the amino acid sequence as set forth in SEQ ID NO:30 and a substantially identical activity as said polypeptide), hybridize under stringent conditions to all or a portion of a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:29 or to all or a portion of a nucleic acid molecule that encodes a polypeptide having the
35 amino acid sequence of SEQ ID NO:30, or are complementary to a *panE* nucleotide sequence as set forth herein.

Additional *ilvB* nucleic acid sequences are those that comprise the nucleotide sequence of SEQ ID NO:31, encode a homologue of the polypeptide having the amino acid sequence set forth in SEQ ID NO:32 (e.g., encode a polypeptide having at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or more identity to the polypeptide having the amino acid sequence as set forth in SEQ ID NO:32 and a substantially identical activity as said polypeptide), hybridize under stringent conditions to all or a portion of a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:31 or to all or a portion of a nucleic acid molecule that encodes a polypeptide having the amino acid sequence of SEQ ID NO:32, or are complementary to an *ilvB* nucleotide sequence as set forth herein.

Additional *ilvN* nucleic acid sequences are those that comprise the nucleotide sequence of SEQ ID NO:33, encode a homologue of the polypeptide having the amino acid sequence set forth in SEQ ID NO:34 (e.g., encode a polypeptide having at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or more identity to the polypeptide having the amino acid sequence as set forth in SEQ ID NO:34 and a substantially identical activity as said polypeptide), hybridize under stringent conditions to all or a portion of a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:33 or to all or a portion of a nucleic acid molecule that encodes a polypeptide having the amino acid sequence of SEQ ID NO:34, or are complementary to an *ilvN* nucleotide sequence as set forth herein.

Additional *ilvC* nucleic acid sequences include those that comprise the nucleotide sequence of SEQ ID NO:35, encode a homologue of the polypeptide having the amino acid sequence set forth in SEQ ID NO:36 (e.g., encode a polypeptide having at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or more identity to the polypeptide having the amino acid sequence as set forth in SEQ ID NO:36 and a substantially identical activity as said polypeptide), hybridize under stringent conditions to all or a portion of a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:35 or to all or a portion of a nucleic acid molecule that encodes a polypeptide having the amino acid sequence of SEQ ID NO:36, or are complementary to an *ilvC* nucleotide sequence as set forth herein.

Additional *ilvD* nucleic acid sequences include those that comprise the nucleotide sequence of SEQ ID NO:37, encode a homologue of the polypeptide having the amino acid sequence set forth in SEQ ID NO:38 (e.g., encode a polypeptide having at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or more identity to the polypeptide having the amino acid sequence as set forth in SEQ ID NO:38 and a substantially identical activity as said polypeptide), hybridize under stringent conditions to all or a portion of a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:37 or

to all or a portion of a nucleic acid molecule that encodes a polypeptide having the amino acid sequence of SEQ ID NO:38, or are complementary to an *ilvD* nucleotide sequence as set forth herein.

Additional *alsS* nucleic acid sequences include those that comprise the
5 nucleotide sequence of SEQ ID NO:86, encode a homologue of the polypeptide having the amino acid sequence set forth in SEQ ID NO:87 (*e.g.*, encode a polypeptide having at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or more identity to the polypeptide having the amino acid sequence as set forth in SEQ ID NO:87 and a substantially identical activity as said polypeptide), hybridize under stringent conditions to all or a
10 portion of a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:86 or to all or a portion of a nucleic acid molecule that encodes a polypeptide having the amino acid sequence of SEQ ID NO:87, or are complementary to an *alsS* nucleotide sequence as set forth herein.

In another embodiment, an isolated nucleic acid molecule is or includes a *coaX*
15 gene, or portion or fragment thereof. In one embodiment, an isolated *coaX* nucleic acid molecule or gene comprises the nucleotide sequence as set forth in SEQ ID NO:19 (*e.g.*, comprises the *B. subtilis coaX* nucleotide sequence). In another embodiment, an isolated *coaX* nucleic acid molecule or gene comprises a nucleotide sequence that encodes the amino acid sequence as set forth in SEQ ID NO:9 (*e.g.*, encodes the *B.*
20 *subtilis* CoaX amino acid sequence). In yet another embodiment, an isolated *coaX* nucleic acid molecule or gene encodes a homologue of the CoaX protein having the amino acid sequence of SEQ ID NO:9. As used herein, the term "homologue" includes a protein or polypeptide sharing at least about 30-35%, preferably at least about 35-40%, more preferably at least about 40-50%, and even more preferably at least about 60%,
25 70%, 80%, 90% or more identity with the amino acid sequence of a wild-type protein or polypeptide described herein and having a substantially equivalent functional or biological activity as said wild-type protein or polypeptide. For example, a CoaX homologue shares at least about 30-35%, preferably at least about 35-40%, more preferably at least about 40-50%, and even more preferably at least about 60%, 70%,
30 80%, 90% or more identity with the protein having the amino acid sequence set forth as SEQ ID NO:9 and has a substantially equivalent functional or biological activity (*i.e.*, is a functional equivalent) of the protein having the amino acid sequence set forth as SEQ ID NO:9 (*e.g.*, has a substantially equivalent pantothenate kinase activity). In a preferred embodiment, an isolated *coaX* nucleic acid molecule or gene comprises a
35 nucleotide sequence that encodes a polypeptide as set forth in any one of SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID

NO:74 or SEQ ID NO:75. In another embodiment, an isolated *coaX* nucleic acid molecule hybridizes to all or a portion of a nucleic acid molecule having the nucleotide sequence set forth in SEQ ID NO:19 or hybridizes to all or a portion of a nucleic acid molecule having a nucleotide sequence that encodes a polypeptide having the amino acid sequence of any of SEQ ID NOs:7-18, 74 or 75. Such hybridization conditions are known to those skilled in the art and can be found in *Current Protocols in Molecular Biology*, Ausubel *et al.*, eds., John Wiley & Sons, Inc. (1995), sections 2, 4 and 6. Additional stringent conditions can be found in *Molecular Cloning: A Laboratory Manual*, Sambrook *et al.*, Cold Spring Harbor Press, Cold Spring Harbor, NY (1989), chapters 7, 9 and 11. A preferred, non-limiting example of stringent hybridization conditions includes hybridization in 4X sodium chloride/sodium citrate (SSC), at about 65-70°C (or hybridization in 4X SSC plus 50% formamide at about 42-50°C) followed by one or more washes in 1X SSC, at about 65-70°C. A preferred, non-limiting example of highly stringent hybridization conditions includes hybridization in 1X SSC, at about 65-70°C (or hybridization in 1X SSC plus 50% formamide at about 42-50°C) followed by one or more washes in 0.3X SSC, at about 65-70°C. A preferred, non-limiting example of reduced stringency hybridization conditions includes hybridization in 4X SSC, at about 50-60°C (or alternatively hybridization in 6X SSC plus 50% formamide at about 40-45°C) followed by one or more washes in 2X SSC, at about 50-60°C. Ranges intermediate to the above-recited values, *e.g.*, at 65-70°C or at 42-50°C are also intended to be encompassed by the present invention. SSPE (1X SSPE is 0.15 M NaCl, 10mM NaH₂PO₄, and 1.25 mM EDTA, pH 7.4) can be substituted for SSC (1X SSC is 0.15 M NaCl and 15 mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes each after hybridization is complete. The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, $T_m(^{\circ}\text{C}) = 2(\# \text{ of A} + \text{T bases}) + 4(\# \text{ of G} + \text{C bases})$. For hybrids between 18 and 49 base pairs in length, $T_m(^{\circ}\text{C}) = 81.5 + 16.6(\log_{10}[\text{Na}^+]) + 0.41(\% \text{G} + \text{C}) - (600/\text{N})$, where N is the number of bases in the hybrid, and $[\text{Na}^+]$ is the concentration of sodium ions in the hybridization buffer ($[\text{Na}^+]$ for 1X SSC = 0.165 M). It will also be recognized by the skilled practitioner that additional reagents may be added to hybridization and/or wash buffers to decrease non-specific hybridization of nucleic acid molecules to membranes, for example, nitrocellulose or nylon membranes, including but not limited to blocking agents (*e.g.*, BSA or salmon or herring sperm carrier DNA), detergents (*e.g.*, SDS), chelating agents (*e.g.*, EDTA), Ficoll, PVP and the like. When using nylon membranes, in particular, an additional preferred, non-limiting example of

stringent hybridization conditions is hybridization in 0.25-0.5M NaH₂PO₄, 7% SDS at about 65°C, followed by one or more washes at 0.02M NaH₂PO₄, 1% SDS at 65°C, see *e.g.*, Church and Gilbert (1984) *Proc. Natl. Acad. Sci. USA* 81:1991-1995, (or, alternatively, 0.2X SSC, 1% SDS). In another preferred embodiment, an isolated
5 nucleic acid molecule comprises a nucleotide sequence that is complementary to a *coaX* nucleotide sequence as set forth herein (*e.g.*, is the full complement of the nucleotide sequence set forth as SEQ ID NO:19).

In another preferred embodiment, an isolated nucleic acid molecule is or includes a *coaA* gene, for example, a *Bacillus* (*e.g.*, *B. subtilis*) *coaA* gene, or portion or
10 fragment thereof. Exemplary isolated *coaA* nucleic acid molecules and/or genes include (1) an isolated *coaA* nucleic acid molecule or gene comprising the nucleotide sequence as set forth in any one of SEQ ID NOs:20-22; (2) an isolated *coaA* nucleic acid molecule or gene comprising a nucleotide sequence that encodes the amino acid sequence as set forth in SEQ ID NO:3; (3) an isolated *coaA* nucleic acid molecule or gene comprising a
15 nucleotide sequence which encodes a CoaA homologue (*e.g.*, a polypeptide having an amino acid sequence at least about 30-35%, preferably at least about 35-40%, more preferably at least about 40-50%, and even more preferably at least about 60%, 70%, 80%, 90% or more identical to the amino acid sequence set forth as SEQ ID NO:3 and having a substantially equivalent enzymatic activity; (4) an isolated *coaA* nucleic acid
20 molecule or gene comprising a nucleotide sequence that encodes a polypeptide as set forth in any one of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:5 or SEQ ID NO:6; (5) an isolated nucleic acid molecule that hybridizes under stringent conditions to all or a portion of a nucleic acid molecule having the nucleotide sequence set forth in SEQ ID NO:20, SEQ ID NO:21 or SEQ ID NO:22 or hybridizes to all or a
25 portion of a nucleic acid molecule having a nucleotide sequence that encodes a polypeptide having the amino acid sequence of SEQ ID NO:3; and (6) an isolated nucleic acid molecule comprising a nucleotide sequence that is complementary to a *coaA* nucleotide sequence as set forth herein (*e.g.*, is the full complement of the nucleotide sequence set forth in SEQ ID NO:20, SEQ ID NO:21 or SEQ ID NO:22).

30 A nucleic acid molecule of the present invention (*e.g.*, a *coaX* nucleic acid molecule or gene or a *coaA* nucleic acid molecule or gene), can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, nucleic acid molecules can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, T.
35 *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989*) or can be isolated by the polymerase chain reaction using synthetic oligonucleotide primers designed

based upon the *coaX* or *coaA* nucleotide sequences set forth herein, or flanking sequences thereof. A nucleic acid of the invention (e.g., a *coaX* nucleic acid molecule or gene or a *coaA* nucleic acid molecule or gene), can be amplified using cDNA, mRNA or alternatively, chromosomal DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques.

Yet another embodiment of the present invention features mutant *coaX* and *coaA* nucleic acid molecules or genes. The phrase "mutant nucleic acid molecule" or "mutant gene" as used herein, includes a nucleic acid molecule or gene having a nucleotide sequence which includes at least one alteration (e.g., substitution, insertion, deletion) such that the polypeptide or protein that may be encoded by said mutant exhibits an activity that differs from the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene. Preferably, a mutant nucleic acid molecule or mutant gene (e.g., a mutant *coaA* or *coaX* gene) encodes a polypeptide or protein having a reduced activity (e.g., having a reduced pantothenate kinase activity) as compared to the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene, for example, when assayed under similar conditions (e.g., assayed in microorganisms cultured at the same temperature). A mutant gene also can encode no polypeptide or have a reduced level of production of the wild-type polypeptide.

As used herein, a "reduced activity" or "reduced enzymatic activity" is one that is at least 5% less than that of the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene, preferably at least 5-10% less, more preferably at least 10-25% less and even more preferably at least 25-50%, 50-75% or 75-100% less than that of the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene. Ranges intermediate to the above-recited values, e.g., 75-85%, 85-90%, 90-95%, are also intended to be encompassed by the present invention. As used herein, a "reduced activity" or "reduced enzymatic activity" also includes an activity that has been deleted or "knocked out" (e.g., approximately 100% less activity than that of the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene).

Activity can be determined according to any well accepted assay for measuring activity of a particular protein of interest. Activity can be measured or assayed directly, for example, measuring an activity of a protein isolated or purified from a cell.

Alternatively, an activity can be measured or assayed within a cell or in an extracellular medium. For example, assaying for a mutant *coaA* gene or a mutant *coaX* gene (i.e., said mutant encoding a reduced pantothenate kinase activity) can be accomplished by expressing the mutated gene in a microorganism, for example, a mutant microorganism which expresses pantothenate kinase in a temperature-sensitive manner, assaying the mutant gene for the ability to complement a temperature sensitive (Ts) mutant for

pantothenate kinase activity. A *coaX* mutant gene or *coaA* mutant gene that encodes a "reduced pantothenate kinase activity" is one that complements the Ts mutant less effectively than, for example, a corresponding wild-type *coaX* gene or *coaA* gene.

It will be appreciated by the skilled artisan that even a single substitution in a nucleic acid or gene sequence (e.g., a base substitution that encodes an amino acid change in the corresponding amino acid sequence) can dramatically affect the activity of an encoded polypeptide or protein as compared to the corresponding wild-type polypeptide or protein. A mutant nucleic acid or mutant gene (e.g., encoding a mutant polypeptide or protein), as defined herein, is readily distinguishable from a nucleic acid or gene encoding a protein homologue, as described above, in that a mutant nucleic acid or mutant gene encodes a protein or polypeptide having an altered activity, optionally observable as a different or distinct phenotype in a microorganism expressing said mutant gene or nucleic acid or producing said mutant protein or polypeptide (i.e., a mutant microorganism) as compared to a corresponding microorganism expressing the wild-type gene or nucleic acid or producing said mutant protein or polypeptide. By contrast, a protein homologue has an identical or substantially similar activity, optionally phenotypically indiscernable when produced in a microorganism, as compared to a corresponding microorganism expressing the wild-type gene or nucleic acid. Accordingly it is not, for example, the degree of sequence identity between nucleic acid molecules, genes, protein or polypeptides that serves to distinguish between homologues and mutants, rather it is the activity of the encoded protein or polypeptide that distinguishes between homologues and mutants: homologues having, for example, low (e.g., 30-50% sequence identity) sequence identity yet having substantially equivalent functional activities, and mutants, for example sharing 99% sequence identity yet having dramatically different or altered functional activities. Exemplary homologues are set forth in Figure 20 (i.e., CoaA homologues) and in Figure 23 (i.e., CoaX homologues). Exemplary mutants are described in Examples XV and XVIII herein.

VIII. Recombinant Nucleic Acid Molecules and Vectors

The present invention further features recombinant nucleic acid molecules (e.g., recombinant DNA molecules) that include nucleic acid molecules and/or genes described herein (e.g., isolated nucleic acid molecules and/or genes), preferably *Bacillus* genes, more preferably *Bacillus subtilis* genes, even more preferably *Bacillus subtilis* pantothenate kinase genes (e.g., *coaX* genes or *coaA* genes), pantothenate biosynthetic genes (e.g., genes encoding pantothenate biosynthetic enzymes, for example, *panB* genes encoding ketopantoate hydroxymethyltransferase, *panE* genes encoding

ketopantoate reductase, *panC* genes encoding pantothenate synthetase, and/or *panD* genes encoding aspartate- α -decarboxylase) and/or isoleucine-valine (*ilv*) biosynthetic genes (e.g., *ilvBN* or *alsS* genes encoding acetohydroxyacid synthetase, *ilvC* genes encoding acetohydroxyacid isomeroreductase and/or *ilvD* genes encoding dihydroxyacid
5 dehydratase).

The present invention further features vectors (e.g., recombinant vectors) that include nucleic acid molecules (e.g., isolated or recombinant nucleic acid molecules and/or genes) described herein. In particular, recombinant vectors are featured that include nucleic acid sequences that encode bacterial gene products as described herein,
10 preferably *Bacillus* gene products, more preferably *Bacillus subtilis* gene products, even more preferably *Bacillus subtilis* pantothenate biosynthetic gene products (e.g., pantothenate biosynthetic enzymes, for example, ketopantoate hydroxymethyltransferase, ketopantoate reductase, pantothenate synthetase, and/or aspartate- α -decarboxylase) and/or isoleucine-valine biosynthetic gene products (e.g.,
15 acetohydroxyacid synthetase, acetohydroxyacid isomeroreductase and/or dihydroxyacid dehydratase).

The term "recombinant nucleic acid molecule" includes a nucleic acid molecule (e.g., a DNA molecule) that has been altered, modified or engineered such that it differs in nucleotide sequence from the native or natural nucleic acid molecule from which the
20 recombinant nucleic acid molecule was derived (e.g., by addition, deletion or substitution of one or more nucleotides). Preferably, a recombinant nucleic acid molecule (e.g., a recombinant DNA molecule) includes an isolated nucleic acid molecule or gene of the present invention (e.g., an isolated *coaX*, *coaA*, *pan* or *ilv* gene) operably linked to regulatory sequences.

The term "recombinant vector" includes a vector (e.g., plasmid, phage, phasmid, virus, cosmid or other purified nucleic acid vector) that has been altered, modified or engineered such that it contains greater, fewer or different nucleic acid sequences than those included in the native or natural nucleic acid molecule from which the
25 recombinant vector was derived. Preferably, the recombinant vector includes a *coaX*, *coaA*, *pan* or *ilv* gene or recombinant nucleic acid molecule including such *coaX*, *coaA*, *pan* or *ilv* gene, operably linked to regulatory sequences, for example, promoter sequences, terminator sequences and/or artificial ribosome binding sites (RBSs), as
30 defined herein.

The phrase "operably linked to regulatory sequence(s)" means that the
35 nucleotide sequence of the nucleic acid molecule or gene of interest is linked to the regulatory sequence(s) in a manner which allows for expression (e.g., enhanced, increased, constitutive, basal, attenuated, decreased or repressed expression) of the

nucleotide sequence, preferably expression of a gene product encoded by the nucleotide sequence (*e.g.*, when the recombinant nucleic acid molecule is included in a recombinant vector, as defined herein, and is introduced into a microorganism).

The term "regulatory sequence" includes nucleic acid sequences which affect (*e.g.*, modulate or regulate) expression of other nucleic acid sequences. In one embodiment, a regulatory sequence is included in a recombinant nucleic acid molecule or recombinant vector in a similar or identical position and/or orientation relative to a particular gene of interest as is observed for the regulatory sequence and gene of interest as it appears in nature, *e.g.*, in a native position and/or orientation. For example, a gene of interest can be included in a recombinant nucleic acid molecule or recombinant vector operably linked to a regulatory sequence which accompanies or is adjacent to the gene of interest in the natural organism (*e.g.*, operably linked to "native" regulatory sequences, for example, to the "native" promoter). Alternatively, a gene of interest can be included in a recombinant nucleic acid molecule or recombinant vector operably linked to a regulatory sequence which accompanies or is adjacent to another (*e.g.*, a different) gene in the natural organism. Alternatively, a gene of interest can be included in a recombinant nucleic acid molecule or recombinant vector operably linked to a regulatory sequence from another organism. For example, regulatory sequences from other microbes (*e.g.*, other bacterial regulatory sequences, bacteriophage regulatory sequences and the like) can be operably linked to a particular gene of interest.

In one embodiment, a regulatory sequence is a non-native or non-naturally-occurring sequence (*e.g.*, a sequence which has been modified, mutated, substituted, derivatized, deleted including sequences which are chemically synthesized). Preferred regulatory sequences include promoters, enhancers, termination signals, anti-termination signals and other expression control elements (*e.g.*, sequences to which repressors or inducers bind and/or binding sites for transcriptional and/or translational regulatory proteins, for example, in the transcribed mRNA). Such regulatory sequences are described, for example, in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989. Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in a microorganism (*e.g.*, constitutive promoters and strong constitutive promoters), those which direct inducible expression of a nucleotide sequence in a microorganism (*e.g.*, inducible promoters, for example, xylose inducible promoters) and those which attenuate or repress expression of a nucleotide sequence in a microorganism (*e.g.*, attenuation signals or repressor sequences). It is also within the scope of the present invention to regulate expression of a gene of interest by removing or deleting regulatory sequences. For

example, sequences involved in the negative regulation of transcription can be removed such that expression of a gene of interest is enhanced.

In one embodiment, a recombinant nucleic acid molecule or recombinant vector of the present invention includes a nucleic acid sequence or gene that encodes at least one bacterial gene product (e.g., a pantothenate biosynthetic enzyme, an isoleucine-valine biosynthetic enzyme, or a CoaA biosynthetic enzyme, for example CoaA or CoaX) operably linked to a promoter or promoter sequence. Preferred promoters of the present invention include *Bacillus* promoters and/or bacteriophage promoters (e.g., bacteriophage which infect *Bacillus*). In one embodiment, a promoter is a *Bacillus* promoter, preferably a strong *Bacillus* promoter (e.g., a promoter associated with a biochemical housekeeping gene in *Bacillus* or a promoter associated with a glycolytic pathway gene in *Bacillus*). In another embodiment, a promoter is a bacteriophage promoter. In a preferred embodiment, the promoter is from the bacteriophage SP01. In a particularly preferred embodiment, a promoter is selected from the group consisting of P_{15} , P_{26} or P_{veg} , for example, the promoters set forth in SEQ ID NO:39, SEQ ID NO:40 or SEQ ID NO:41. Additional preferred promoters include *tef* (the translational elongation factor (TEF) promoter) and *pyc* (the pyruvate carboxylase (PYC) promoter), which promote high level expression in *Bacillus* (e.g., *Bacillus subtilis*). Additional preferred promoters, for example, for use in Gram positive microorganisms include, but are not limited to, the *amyE* promoter or phage SP02 promoters. Additional preferred promoters, for example, for use in Gram negative microorganisms include, but are not limited to *tac*, *trp*, *tet*, *trp-tet*, *lpp*, *lac*, *lpp-lac*, *lacIq*, *T7*, *T5*, *T3*, *gal*, *trc*, *ara*, λ - P_R or λ - P_L .

In another embodiment, a recombinant nucleic acid molecule or recombinant vector of the present invention includes a terminator sequence or terminator sequences (e.g., transcription terminator sequences). The term "terminator sequences" includes regulatory sequences which serve to terminate transcription of a gene. Terminator sequences (or tandem transcription terminators) can further serve to stabilize mRNA (e.g., by adding structure to mRNA), for example, against nucleases.

In yet another embodiment, a recombinant nucleic acid molecule or recombinant vector of the present invention includes sequences which allow for detection of the vector containing said sequences (i.e., detectable and/or selectable markers), for example, sequences that overcome auxotrophic mutations, for example, *ura3* or *ilvE*, fluorescent markers, and/or colorimetric markers (e.g., *lacZ*/ β -galactosidase), and/or antibiotic resistance genes (e.g., *amp* or *tet*).

In yet another embodiment, a recombinant nucleic acid molecule or recombinant vector of the present invention includes an artificial ribosome binding site (RBS). The term "artificial ribosome binding site (RBS)" includes a site within an mRNA molecule (e.g., coded within DNA) to which a ribosome binds (e.g., to initiate translation) which differs from a native RBS (e.g., a RBS found in a naturally-occurring gene) by at least one nucleotide. Preferred artificial RBSs include about 5-6, 7-8, 9-10, 11-12, 13-14, 15-16, 17-18, 19-20, 21-22, 23-24, 25-26, 27-28, 29-30 or more nucleotides of which about 1-2, 3-4, 5-6, 7-8, 9-10, 11-12, 13-15 or more differ from the native RBS (e.g., the native RBS of a gene of interest). Preferably, nucleotides which differ are substituted such that they are identical to one or more nucleotides of an ideal RBS (e.g., SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47 or SEQ ID NO:48), when optimally aligned for comparisons. Artificial RBSs can be used to replace the naturally-occurring or native RBS associated with a particular gene. Artificial RBSs preferably increase translation of a particular gene. Preferred artificial RBSs (e.g., RBSs for increasing the translation of *panB*, for example, of *B. subtilis panB*) are depicted in Table 1A (e.g., SEQ ID NO:49 and SEQ ID NO:50).

Table 1A: Preferred *panB* Ribosome Binding Sites

20	10	20	
	-----AGAAAGGAGGTGA		ideal RBS (SEQ ID NO:44)
	CCCTCT-AG-AAGGAGGAGAAAACATG		RBS1 (SEQ ID NO:49)
	CCCTCT-AG--AGGAGGAGAAAACATG		RBS2 (SEQ ID NO:50)
25	TAAACAT-G--AGGAGGAGAAAACATG		panB native RBS (SEQ ID NO:42)

Additional preferred artificial RBSs (e.g., RBSs for increasing the translation of *panD*, for example, of *B. subtilis panD*) are depicted in Table 1B (e.g., SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53 and SEQ ID NO:54).

Table 1B: Preferred *panD* Ribosome Binding Sites

35	10	20	
	CTAGAAAAGGAGGAATTTAAATG		pAN423 RBS (SEQ ID NO:88)
	TTAAGAAAGGAGGTGANNNNATG		ideal RBS (SEQ ID NO:45)
	TTAGAAAGGAGGATTTAAATATG		new design A (SEQ ID NO:51)
	TTAGAAAGGAGGTTTAATTAATG		new design B (SEQ ID NO:52)
40	TTAGAAAGGAGGTGATTTAAATG		new design C1 (SEQ ID NO:53)
	TTAGAAAGGAGGTGTTTAAATG		new design C2 (SEQ ID NO:54)
	TTAGAAAGGAGGTGANNNNATG		ideal RBS (SEQ ID NO:46)

Additional preferred artificial RBSs (*e.g.*, RBSs for increasing the translation of *panD*, for example, of *B. subtilis panD*) are depicted in Table 1C (*e.g.*, SEQ ID NO:55, SEQ ID NO:56 and SEQ ID NO:57). The predicted amino acid sequence at the C-terminus of the PanC protein is shown. The start codon for PanD translation is underlined.

Table 1C: Additional Preferred *panD* Ribosome Binding Sites

	10	20	
10	---	--A GAA AGG AGG TGA NNN NNN N <u>ATG</u>	ideal RBS (SEQ ID NO:47)
	ATT CGA GAA ATG GAG AGA ATA TAA T <u>ATG</u>		native <i>panD</i> RBS (SEQ ID NO:43)
	Ile Arg Glu Met Glu Arg Ile *	Met	SEQ ID NO:89
15	---	--A GAA AGG AGG TGA NNN NNN N <u>ATG</u>	ideal RBS (SEQ ID NO:47)
	ATT CGA GAA AGG AGG TGA ATA TAA T <u>ATG</u>		NDI (SEQ ID NO:55)
	Ile Arg Glu Arg Arg *	Met	SEQ ID NO:90
20	ATT CGA GAA AGG AGG TGA ATA ATA - <u>ATG</u>		NDII (SEQ ID NO:56)
	Ile Arg Glu Arg Arg *	Met	SEQ ID NO:90
	ATT CGT AGA AAG GAG GTG AAT TAA T <u>ATG</u>		NDIII (SEQ ID NO:57)
25	Ile Arg Arg Lys Glu Val Asn *	Met	SEQ ID NO:91
	---	--- AGA AAG GAG GTG ANN NNN N <u>ATG</u>	ideal RBS (SEQ ID NO:48)

Accordingly, in one embodiment, a vector of the present invention includes an artificial RBS as set forth in SEQ ID NO:49 or SEQ ID NO:50. In another embodiment, a vector of the present invention includes an artificial RBS as set forth in SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53 or SEQ ID NO:54. In yet another embodiment, a vector of the present invention includes an artificial RBS as set forth in SEQ ID NO:55, SEQ ID NO:56 or SEQ ID NO:57.

In another embodiment, a recombinant vector of the present invention includes sequences that enhance replication in bacteria (*e.g.*, replication-enhancing sequences). In one embodiment, replication-enhancing sequences are derived from *E. coli*. In another embodiment, replication-enhancing sequences are derived from pBR322 (*e.g.*, sequences included within the pBR322 derived portion of any of the pAN vectors as set forth in the Figures, *i.e.*, the Not I-Not I sequences from about 5.0 kB to 9.0 kB of the vector depicted in Figure 3A).

In yet another embodiment, a recombinant vector of the present invention includes antibiotic resistance genes. The term "antibiotic resistance genes" includes sequences which promote or confer resistance to antibiotics on the host organism (*e.g.*, *Bacillus*). In one embodiment, the antibiotic resistance genes are selected from the group consisting of *cat* (chloramphenicol resistance) genes, *tet* (tetracycline resistance) genes, *erm* (erythromycin resistance) genes, *neo* (neomycin resistance) genes and *spec* (spectinomycin resistance) genes. Recombinant vectors of the present invention can further include homologous recombination sequences (*e.g.*, sequences designed to allow recombination of the gene of interest into the chromosome of the host organism). For example, *amyE* sequences can be used as homology targets for recombination into the host chromosome.

Preferred vectors of the present invention include, but are not limited to, vectors set forth in Figures 2-15, 17, 19, 22, 25 and 26. It will further be appreciated by one of skill in the art that the design of a vector can be tailored depending on such factors as the choice of microorganism to be genetically engineered, the level of expression of gene product desired and the like.

IX. Isolated Proteins

Another aspect of the present invention features isolated proteins (*e.g.*, isolated pantothenate biosynthetic enzymes and/or valine-isoleucine biosynthetic enzymes and/or isolated CoA biosynthetic enzymes, for example isolated CoaA or CoaX). In one embodiment, proteins (*e.g.*, isolated pantothenate biosynthetic enzymes and/or valine-isoleucine biosynthetic enzymes and/or isolated CoaA biosynthetic enzymes, for example isolated CoaA or CoaX) are produced by recombinant DNA techniques and can be isolated from microorganisms of the present invention by an appropriate purification scheme using standard protein purification techniques. In another embodiment, proteins are synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein (*e.g.*, an isolated or purified biosynthetic enzyme) is substantially free of cellular material or other contaminating proteins from the microorganism from which the protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. In one embodiment, an isolated or purified protein has less than about 30% (by dry weight) of contaminating protein or chemicals, more preferably less than about 20% of contaminating protein or chemicals, still more preferably less than about 10% of contaminating protein or chemicals, and most preferably less than about 5% contaminating protein or chemicals.

In a preferred embodiment, the protein or gene product is derived from *Bacillus* (e.g., is *Bacillus*-derived). The term "derived from *Bacillus*" or "*Bacillus*-derived" includes a protein or gene product which is encoded by a *Bacillus* gene. Preferably, the gene product is derived from a microorganism selected from the group consisting of

5 *Bacillus subtilis*, *Bacillus lentimorbus*, *Bacillus lentus*, *Bacillus firmus*, *Bacillus pantothenicus*, *Bacillus amyloliquefaciens*, *Bacillus cereus*, *Bacillus circulans*, *Bacillus coagulans*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus thuringiensis*, and other Group 1 *Bacillus* species, for example, as characterized by 16S rRNA type (Priest, *supra*). In another preferred embodiment, the protein or gene

10 product is derived from *Bacillus brevis* or *Bacillus stearothermophilus*. In another preferred embodiment, the protein or gene product is derived from a microorganism selected from the group consisting of *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus halodurans*, *Bacillus subtilis*, and *Bacillus pumilus*. In a particularly preferred embodiment, the protein or gene product is derived from *Bacillus subtilis* (e.g., is

15 *Bacillus subtilis*-derived). The term "derived from *Bacillus subtilis*" or "*Bacillus subtilis*-derived" includes a protein or gene product which is encoded by a *Bacillus subtilis* gene. In yet another preferred embodiment, the protein or gene product is encoded by a *Bacillus* gene homologue (e.g., a gene derived from a species distinct from *Bacillus* but having significant homology to a *Bacillus* gene of the present invention, for

20 example, a *Bacillus pan* gene or *Bacillus ilv* gene).

Included within the scope of the present invention are bacterial-derived proteins or gene products and/or *Bacillus*-derived proteins or gene products (e.g., *B. subtilis*-derived gene products) that are encoded by naturally-occurring bacterial and/or *Bacillus* genes (e.g., *B. subtilis* genes), for example, the genes identified by the present inventors,

25 for example, *Bacillus* or *B. subtilis coaX* genes, *coaA* genes, *pan* genes and/or *ilv* genes. Further included within the scope of the present invention are bacterial-derived proteins or gene products and/or *Bacillus*-derived proteins or gene products (e.g., *B. subtilis*-derived gene products) that are encoded bacterial and/or *Bacillus* genes (e.g., *B. subtilis* genes) which differ from naturally-occurring bacterial and/or *Bacillus* genes (e.g., *B.*

30 *subtilis* genes), for example, genes which have nucleic acids that are mutated, inserted or deleted, but which encode proteins substantially similar to the naturally-occurring gene products of the present invention. For example, it is well understood that one of skill in the art can mutate (e.g., substitute) nucleic acids which, due to the degeneracy of the genetic code, encode for an identical amino acid as that encoded by the naturally-

35 occurring gene. Moreover, it is well understood that one of skill in the art can mutate (e.g., substitute) nucleic acids which encode for conservative amino acid substitutions. It is further well understood that one of skill in the art can substitute, add or delete

amino acids to a certain degree without substantially affecting the function of a gene product as compared with a naturally-occurring gene product, each instance of which is intended to be included within the scope of the present invention.

In a preferred embodiment, an isolated protein of the present invention (*e.g.*, an isolated pantothenate biosynthetic enzyme and/or an isolated isoleucine-valine biosynthetic enzyme and/or an isolated CoaA biosynthetic enzymes, for example isolated CoaA or CoaX) has an amino acid sequence shown in SEQ ID NO:3, SEQ ID NO:9, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38 or SEQ ID NO:87. In other embodiments, an isolated protein of the present invention is a homologue of the at least one of the proteins set forth as SEQ ID NO:3, SEQ ID NO:9, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38 or SEQ ID NO:87 (*e.g.*, comprises an amino acid sequence at least about 30-40% identical, preferably about 40-50% identical, more preferably about 50-60% identical, and even more preferably about 60-70%, 70-80%, 80-90%, 90-95% or more identical to the amino acid sequence of SEQ ID NO:3, SEQ ID NO:9, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38 or SEQ ID NO:87, and has an activity that is substantially similar to that of the protein encoded by the amino acid sequence of SEQ ID NO:3, SEQ ID NO:9, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38 or SEQ ID NO:87, respectively.

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = # of identical positions/total # of positions x 100), preferably taking into account the number of gaps and size of said gaps necessary to produce an optimal alignment.

The comparison of sequences and determination of percent homology between two sequences can be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-77. Such

an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Research* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov>. Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller (1988) *Comput Appl Biosci.* 4:11-17. Such an algorithm is incorporated into the ALIGN program available, for example, at the GENESTREAM network server, IGH Montpellier, FRANCE (<http://vega.igh.cnrs.fr>) or at the ISREC server (<http://www.ch.embnet.org>). When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

In another preferred embodiment, the percent homology between two amino acid sequences can be determined using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. In yet another preferred embodiment, the percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using a gap weight of 50 and a length weight of 3.

25

X. Biotransformations and Bioconversions

Another aspect of the present invention includes biotransformation processes which feature recombinant microorganisms (*e.g.*, mutant microorganisms) and/or isolated CoA, pantothenate or isoleucine-valine biosynthetic enzymes described herein. The term "biotransformation process", also referred to herein as "bioconversion processes", includes biological processes which result in the production (*e.g.*, transformation or conversion) of any compound (*e.g.*, intermediate or product) which is upstream of a CoA, pantothenate or isoleucine-valine biosynthetic enzyme to a compound (*e.g.*, substrate, intermediate or product) which is downstream of said CoA, pantothenate or isoleucine-valine biosynthetic enzyme.

35

In one embodiment, the invention features a biotransformation process for the production of a panto-compound comprising contacting a microorganism which overexpresses at least one pantothenate biosynthetic enzyme with at least one appropriate substrate or precursor under conditions such that said panto-compound is produced and recovering said panto-compound. In a preferred embodiment, the invention features a biotransformation process for the production of pantoate comprising contacting a microorganism which overexpresses ketopantoate reductase (the *panE* gene product) with an appropriate substrate (e.g., ketopantoate) under conditions such that pantoate is produced and recovering said pantoate. In another preferred embodiment, the invention features a biotransformation process for the production of pantothenate comprising contacting a microorganism which overexpresses ketopantoate reductase and pantothenate synthetase with appropriate substrates (e.g., ketopantoate and β -alanine) under conditions such that pantothenate is produced and recovering said pantothenate. In yet another preferred embodiment, the invention features a biotransformation process for the production of pantothenate comprising contacting a microorganism which overexpresses ketopantoate hydroxymethyltransferase, ketopantoate reductase and pantothenate synthetase with appropriate substrates (e.g., α -ketoisovalerate and β -alanine) under conditions such that pantothenate is produced and recovering said pantothenate. Preferred recombinant microorganisms for carrying out the above-described biotransformations include pantothenate kinase mutants. Conditions under which pantoate or pantothenate are produced can include any conditions which result in the desired production of pantoate or pantothenate, respectively.

In yet another embodiment, the present invention includes a method of producing β -alanine that includes culturing a microorganism which overexpresses aspartate- α -decarboxylase under conditions such that β -alanine is produced. Preferably, the aspartate- α -decarboxylase-overexpressing microorganism has a mutation in a nucleic acid sequence encoding a pantothenate biosynthetic enzyme selected from the group consisting of ketopantoate hydroxymethyltransferase, ketopantoate reductase and pantothenate synthetase.

The invention further features a method of producing β -alanine that includes contacting a composition comprising aspartate with an isolated *Bacillus* aspartate- α -decarboxylase enzyme under conditions such that β -alanine is produced (e.g., an *in vitro* synthesis method).

The microorganism(s) and/or enzymes used in the biotransformation reactions are in a form allowing them to perform their intended function (e.g., producing a desired compound). The microorganisms can be whole cells, or can be only those portions of the cells necessary to obtain the desired end result. The microorganisms can be

suspended (*e.g.*, in an appropriate solution such as buffered solutions or media), rinsed (*e.g.*, rinsed free of media from culturing the microorganism), acetone-dried, immobilized (*e.g.*, with polyacrylamide gel or k-carrageenan or on synthetic supports, for example, beads, matrices and the like), fixed, cross-linked or permeablized (*e.g.*, have permeablized membranes and/or walls such that compounds, for example, substrates, intermediates or products can more easily pass through said membrane or wall).

Purified or unpurified CoA biosynthetic enzyme(s) (*e.g.*, CoaA and/or CoaX), pantothenate biosynthetic enzyme(s) and/or valine-isoleucine biosynthetic enzyme(s) can also be used in biotransformation reactions. The enzyme can be in a form that allows it to perform its intended function (*e.g.*, obtaining the desired compound). For example, the enzyme can be in free form or immobilized. Purified or unpurified CoA biosynthetic enzyme(s), pantothenate biosynthetic enzyme(s) and/or valine-isoleucine biosynthetic enzyme(s) can be contacted in one or more *in vitro* reactions with appropriate substrate(s) such that the desired product is produced.

With respect to at least the above-described methodologies (*e.g.*, the production methodologies of the present invention), at least one aspect of the invention features the following: embodiments in which the methods do not use microorganisms of the genus *Corynebacterium* and/or microorganisms of the genus *Escherichia*; embodiments in which the methods do not use microorganisms selected from the group consisting of *Escherichia coli* and *Corynebacterium glutamicum*; embodiments in which the methods do not use gram negative microorganisms; embodiments in which the microorganisms utilized do not include, express or produce nucleic acid molecules, genes or proteins (*e.g.*, biosynthetic enzymes) derived from microorganisms of the genus *Corynebacterium* and/or microorganisms of the genus *Escherichia*; embodiments in which the microorganisms do not include, express or produce nucleic acid molecules, genes or proteins (*e.g.*, biosynthetic enzymes) derived from microorganisms selected from the group consisting of *Escherichia coli* and *Corynebacterium glutamicum*.

XI. Screening Assays

Because CoA is an essential factor in bacteria, proteins (*e.g.*, enzymes) involved in the biosynthesis of CoA provide valuable tools in the search for novel anti-biotics. In particular, the CoaX protein is a valuable target for identifying bacteriocidal compounds because it bears no resemblance in primary sequence to mammalian pantothenate kinase enzymes. Accordingly, the present invention also provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, small molecules or other drugs)

which bind to CoaX, or have a stimulatory or inhibitory effect on, for example, *coaX* expression or CoaX activity.

In one embodiment, the invention provides assays for screening candidate or test compounds which are capable of binding to CoaX proteins or a biologically active portion thereof. In another embodiment, the invention provides assays for screening candidate or test compounds which modulate the activity of CoaX proteins or biologically active portions thereof. The test compounds of the present invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S. (1997) *Anticancer Drug Des.* 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc. Natl. Acad. Sci. U.S.A.* 90:6909; Erb, *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:11422; Zuckermann *et al.* (1994). *J. Med. Chem.* 37:2678; Cho *et al.* (1993) *Science* 261:1303; Carrell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2059; Carrell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2061; and in Gallop *et al.* (1994) *J. Med. Chem.* 37:1233. Libraries of compounds may be presented in solution (*e.g.*, Houghten (1992) *Biotechniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), chips (Fodor (1993) *Nature* 364:555-556), bacteria (Ladner USP 5,223,409), spores (Ladner USP '409), plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and Smith (1990) *Science* 249:386-390); (Devlin (1990) *Science* 249:404-406); (Cwirla *et al.* (1990) *Proc. Natl. Acad. Sci.* 87:6378-6382); (Felici (1991) *J. Mol. Biol.* 222:301-310); (Ladner *supra.*).

In one embodiment, an assay is a microorganism-based assay in which a recombinant microorganism which expresses a CoaX protein or biologically active portion thereof is contacted with a test compound and the ability of the test compound to modulate CoaX activity is determined. Determining the ability of the test compound to modulate CoaX activity can be accomplished by monitoring, for example, intracellular phosphopantoate or CoA concentrations or secreted pantothenate concentrations (as compounds that inhibit CoaX will result in a buildup of pantothenate in the test microorganism). CoaX substrate can be labeled with a radioisotope or enzymatic label such that modulation of CoaX activity can be determined by detecting a conversion of labeled substrate to intermediate or product. For example, CoaX substrates can be

labeled with ^{32}P , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Determining the ability of a compound to modulate CoaX activity can alternatively be determined by detecting the induction of a reporter gene (comprising a CoA-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a CoA-regulated cellular response.

In yet another embodiment, a screening assay of the present invention is a cell-free assay in which a CoaX protein or biologically active portion thereof is contacted with a test compound *in vitro* and the ability of the test compound to bind to or modulate the activity of the CoaX protein or biologically active portion thereof is determined. In a preferred embodiment, the assay includes contacting the CoaX protein or biologically active portion thereof with known substrates to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to modulate enzymatic activity of the CoaX on its substrates.

Screening assays can be accomplished in any vessel suitable for containing the microorganisms, proteins, and/or reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either CoaX protein or a recombinant microorganism expressing CoaX protein to facilitate separation of products and/or substrates, as well as to accommodate automation of the assay. For example, glutathione-S-transferase/CoaX fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates. Other techniques for immobilizing proteins on matrices (*e.g.*, biotin-conjugation and streptavidin immobilization or antibody conjugation) can also be used in the screening assays of the invention.

In another embodiment, modulators of CoaX expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of *coaX* mRNA or CoaX polypeptide in the cell is determined. The level of expression in the presence of the candidate compound is compared to the level of expression in the absence of the candidate compound (or to a suitable control, for example, an appropriate buffer control or standard). The candidate compound can then be identified as a modulator of *coaX* mRNA or CoaX polypeptide expression based on this comparison.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an CoaX modulating agent identified as described herein (*e.g.*, an anti-bactericidal

compound) can be used in an infectious animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patents, patent applications
5 (including U.S. Patent Application Serial No. 09/400,494, filed September 21, 1999 (pending), provisional U.S. Patent Application Serial No. 60/210,072, filed June 7, 2000, provisional U.S. Patent Application Serial No. 60/221,938, filed July 28, 2000 and provisional U.S. Patent Application Serial No. 60/227,860, filed August 24, 2000, to which this application relates) and published patent applications cited throughout this
10 application are incorporated herein by reference.

EXAMPLES

General Methodology:

Strains. *Bacillus subtilis* strains of the present invention are generally derived from either of two strains. The first is variously named "168", "1A1", or "RL-1". The genotype is *trpC2*. This strain was derived from the wild type "Marburg" strain by mutagenesis and has been the basis of much of the molecular biology work done on *B. subtilis*. The second strain is PY79, a prototrophic derivative of 168 that was made Trp⁺ by transduction from the wild type strain W23.

Media. Standard minimal medium for *B. subtilis* is comprised of 1 x Spizizen salts and 0.5% glucose. Standard solid "rich medium" is Tryptone Blood Agar Broth (Difco), and standard liquid "rich medium" is VY, a mixture of veal infusion broth and yeast extract. For testing production of pantothenate in liquid test tube cultures, an enriched form of VY, called "Special VY" or "SVY" is used. For batch fermentations, SVYG and PFMG are used. The compositions of these media are given below.

VY, a rich liquid medium: 25 g Difco Veal Infusion Broth, 5 g Difco Yeast Extract, 1L water (autoclave).

TBAB, a rich solid medium: 33 g Difco Tryptone Blood Agar Broth, 1L water (autoclave).

MIN, a minimal medium: 100 ml 10 x Spizizen salts; 10 ml 50% glucose; 2 ml 10% arginine HCl*; 10 ml 0.8% tryptophan**; water to 1 liter. (*In some cases, arginine is omitted or replaced by sodium glutamate at 0.04% final concentration. In general, *B. subtilis* grows faster in minimal medium when certain amino acids, such as arginine, glutamine, glutamate, or proline, are added as an auxiliary nitrogen source.) (**For strains that are tryptophan auxotrophs, tryptophan is routinely added to most minimal media.)

10 x Spizizen Salts: 174 g $K_2HPO_4 \cdot 3H_2O$; 20 g $(NH_4)_2SO_4$; 60 g KH_2PO_4 ; 10 g $Na_3Citrate \cdot 2H_2O$; 2 g $MgSO_4 \cdot 7H_2O$; water to 993 mls; then add 3.5 ml $FeCl_3$ solution and 3.5 ml Trace Elements solution.

$FeCl_3$ Solution: 4 g $FeCl_3 \cdot 6H_2O$; 197 g $Na_3Citrate \cdot 2H_2O$; water to 1 liter (filter sterilize)

Trace Elements Solution: 0.15 g $Na_2MoO_4 \cdot 2H_2O$; 2.5 g H_3BO_3 ; 0.7 g $CoCl_2 \cdot 6H_2O$; 0.25 g $CuSO_4 \cdot 5H_2O$; 1.6 g $MnCl_2 \cdot 4H_2O$; 0.3 g $ZnSO_4 \cdot 7H_2O$; water to 1 liter (filter sterilize).

SVY, Special VY, a supplemented rich medium for testing pantothenate production in test tube cultures:* 25 g Difco Veal Infusion Broth; 5 g Difco yeast extract; 5 g sodium glutamate; 2.7 g ammonium sulfate; 740 ml water (autoclave); add 200 ml 1 M potassium phosphate, pH 7.0; 60 ml 50% glucose. (*For testing pantothenate production in liquid SVY test tube cultures, Na α -ketoisovalerate and/or β -alanine can be added to a concentration of 5 g/L from filter-sterilized stocks.)

PFMG, a yeast extract based medium used in fermentors: 20 g Amberex 1003™ yeast extract; 5 g sodium glutamate, 2 g ammonium sulfate; 5 g tryptophan; 10 g KH_2PO_4 ; 20 g $\text{K}_2\text{HPO}_4 \cdot 3\text{H}_2\text{O}$; 1 g $\text{MgCl}_2 \cdot 6\text{H}_2\text{O}$; 0.1 g $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$; 1 g sodium citrate; 0.01 g $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$; 1 ml trace elements solution; 20 g glucose; add water to 1 L. Glucose or other sugars are fed as needed. Feed solutions can contain minerals, defined or food grade nutrients.

PF, a chemically defined pantothenate free medium for testing pantothenate auxotrophy: 100 ml 10 x Spizizen Salts; 100 ml 1 x Difco Pantothenate Assay Medium; 10 ml 50% glucose; water to 1 liter.

For pantothenate auxotrophs, 1 mM Na pantothenate is added to both minimal and rich media, since there is generally not enough pantothenate in rich media to support *B. subtilis pan* mutants. Amino acids are at 100 mg per liter, when used. Selection for antibiotic resistance is done with 5 mg/L chloramphenicol, 100 mg/L spectinomycin HCl, 15 mg/L tetracycline HCl, or 1 mg/L erythromycin plus 25 mg/L lincomycin.

Pantothenate Assays: Biological assay. The indicator organism, *Lactobacillus plantarum*, requires pantothenate for growth, and responds to low concentrations ($\mu\text{g/L}$). Thus, using serial dilutions, a wide range of concentrations can be assayed. Commercially available medium (e.g., Pantothenate Assay Medium (PAM), Difco), can be used. However, Difco PAM supplemented with pantothenate does not support growth to the same level as obtainable using a fresh-mixed version of Pantothenate Assay Medium (FM-PAM), made up of the individual components as specified by Difco, which is accordingly, routinely used instead of the commercial product.

Before assaying *B. subtilis* culture supernatants, the *B. subtilis* cells must be either removed or killed. *B. subtilis* culture supernatants give approximately the same pantothenate titer when the supernatants are autoclaved as when they are sterile filtered. Accordingly, routine procedures involve autoclaving samples for 5 minutes prior to the biological assay.

Pantothenate Assays : HPLC assay. Pantothenic acid production is measured by HPLC with a detector wavelength of 197 nm and a reference at 450 nm. The procedure is a modification of one recommended by Hewlett-Packard for water soluble vitamins. Samples of culture broth are diluted into an equal volume of 60% acetonitrile (ACN), centrifuged and filtered. Typically a further 10-fold dilution before analysis brings the final dilution to 20-fold. Higher concentrations of product are diluted further. Compounds are separated on a C18 Phenomenex 5 μ Aqua 250 x 4.6 mm column with 5% acetonitrile (ACN) in 50 mM Na phosphate buffer at pH 2.5. An ACN gradient from 5% to 95% washes the column between every sample. The area of the pantothenate peak is proportional to the concentration between 5 to 1000 mg/L. Other panto-compounds are also separated and quantitated by this method.

Amino Acid Analysis: HPLC assay. Amino acids present in the fermentation medium and throughout the fermentation are measured by HPLC with a detector wavelength of 338 nm and a reference at 390 nm. The procedure is a modification of one recommended by Hewlett-Packard for amino acid analysis. Samples of culture broth are prepared identically as for the panto-compound analysis. Compounds are separated on a C18 Hypersil 5 μ ODS 200 x 2.1 mm column. Solvent A is 20 mM Na acetate buffer at pH 7.2. Solvent B contains 40% ACN and 40% methanol. A gradient from 100% Solvent A to 100% Solvent B separates amino acids and washes the column between every sample.

Batch Fermentations. Pantothenate producing strains are grown in stirred tank fermentors, for example, in CF3000 Chemap 14 liter vessels with 10 liter working volumes. Computer control and data collection is by commercial software, for example, B. Braun Biotech MFCS software. Fermentations can be batch processes but are preferably sugar-limited, fed batch processes. Some media components (e.g. of SVYG and PMFG) are added to the fermentor and sterilized in place. Portions of the media are sterilized separately and added to the fermentors aseptically. This procedure is well known to those familiar with the art. Additional nitrogen sources in feeds are sterilized separately and added to the carbon source after cooling.

The initial sugar in the medium is consumed in approximately 6 hours. Afterwards, glucose or other sugars are fed with the possible addition of minerals, and defined or food grade nutrients. Alternatively, feeds are scheduled based on a consensus profile of nutritional requirements from samples taken from earlier fermentations.

After inoculation, agitation is set at a relatively low speed, e.g. 200 rpm. When the dissolved oxygen (pO₂) falls to 30%, computer control automatically adjusts the agitation to maintain a dissolved oxygen concentration between 25 and 30% pO₂.

5 **EXAMPLE I: Enhanced Production of a Panto-Compound Using Bacteria Overexpressing *panBCD* Gene Products.**

This Example describes the cloning of the *B. subtilis panBCD* operon and the generation of microorganisms overexpressing the *panBCD* gene products.

To clone the *B. subtilis panBCD* operon, a plasmid library of *B. subtilis* GP275
10 (a derivative of 168) genomic DNA was transformed in *E. coli* BM4062 (*birA*^{ts}), and temperature resistant clones were selected at 42°C. By comparison of restriction maps to the genome sequence, one particular clone was deduced to contain the *B. subtilis birA* gene and the adjacent *panBCD* genes. This plasmid was named pAN201.

To overexpress the *panBCD* operon and produce pantothenate, the native
15 promoter of the *panBCD* operon was replaced by either of two strong, constitutive promoters derived from the *B. subtilis* bacteriophage SP01. These two promoters are named *P*₂₆ and *P*₁₅. In addition, either of two artificial ribosome binding sites (RBSs) were used to replace the native *panB* RBS. These two artificial RBSs (set forth as SEQ ID NO:49 and SEQ ID NO:50) were predicted to increase translation of *panBCD*; their
20 sequences are shown in Table 1A. Three such engineered *panBCD* expression cassettes were built into circular plasmids capable of replicating in *E. coli*. Other features of the plasmids include a strong rho-independent transcription terminator from the *E. coli* ribosomal RNA transcription unit, called T₁T₂, a Gram-positive chloramphenicol resistance gene (*cat*), derived from pC194, and a pair of *NotI* restriction sites at the
25 junctions between the *E. coli* replicon and the segment intended for integration into *B. subtilis*. Three plasmids of this series, pAN004, pAN005, and pAN006 were constructed. pAN004 contains the *P*₂₆ promoter, RBS1, and a low copy *E. coli* replicon. pAN005 contains the *P*₁₅ promoter, which in our experience is not as strong as *P*₂₆, RBS1, and the low copy replicon. pAN006 contains the *P*₂₆ promoter, RBS2, and a
30 medium copy replicon.

The three *panBCD* expression cassettes contained in the above-mentioned three plasmids were all ligated to a DNA fragment consisting of sequences that naturally occur immediately upstream from the native *panB* gene and integrated in single copy by homologous recombination into the *panBCD* locus of *B. subtilis* strains RL-1 and PY79,
35 replacing the wild-type operon. This was accomplished in two steps. First a deletion-substitution that replaced about two thirds of the *panB* coding region with a Gram-

positive spectinomycin resistance gene (*spec*) was integrated at *panB* to yield *Spec^r*, pantothenate auxotrophs. These intermediate strains were then transformed with the *panBCD* expression cassettes of pAN004, pAN005, and pAN006 after ligating them to a DNA fragment containing chromosomal sequences just upstream of *panB*. Selection of the incoming cassette was for pantothenate prototrophy. The resulting strains were named PA221, PA222 and PA223 (from RL-1), and PA235, PA232 and PA233 (from PY79), respectively. An example of a plasmid that contains the joined upstream sequence that is in the integrated strain in PA221 is pAN240 (see Figure 2). The nucleotide sequence of pAN240 is set forth as SEQ ID NO:76.

10 Polymerase chain reaction using appropriate primers was used to verify the correct chromosomal structures of these engineered strains. When extracts of strain PA221 were examined by SDS-PAGE, two proteins were found to be overexpressed. One protein had an apparent molecular weight of 29,000 and the other protein appeared to be 39,000 daltons. The 29,000 dalton bands is presumably PanB (predicted molecular weight of 29,761). The larger protein band presumably represents PanC (predicted size 31,960 daltons).

The ability of these strains to produce pantothenate in test tube cultures was assessed as follows. Each strain was grown in SVY medium supplemented with 5 g/L α -ketoisovalerate (α -KIV) and 5 g/L β -alanine, to ensure that these precursors were not limiting. Culture supernatants were autoclaved and assayed using the bioassay. Relative to the parent strains, RL-1 and PY79, the engineered strains produced about 8- to 30-fold more pantothenate, attaining 1 g/L pantothenate in some cases.

Table 2. *Production of pantothenate by engineered B. subtilis strains in liquid test tube cultures grown in SVY medium with 5 g/L α -KIV and 5 g/L β -alanine.*

Expt.	Strain	Promoter	RBS at <i>panB</i>	[pantothenate] mg/L
1	RL-1	Native	Native	30
	PA221	P_{26}	RBS1	990
				790
	PA222	P_{15}	RBS1	250
				250
	PA223	P_{26}	RBS2	790
				790
2	PY79	Native	Native	40
	PA235	P_{26}	RBS1	930
				860
	PA221	P_{26}	RBS1	1100
				1030

- 5 The P_{26} promoter was about 3- to 4-fold more effective than the P_{15} promoter, while RBS1 and RBS2 were roughly equivalent. Plasmids such as pAN004, pAN005, pAN006 can also be recombined as circles into the *B. subtilis* wild type *panBCD* locus by Campbell-type (single crossover) integration, selecting for chloramphenicol resistance at 5 mg/L. Strains obtained in this fashion produce about the same amount of
- 10 pantothenate as strains PA221, PA222, and PA223, respectively. pAN004 containing the P_{26} promoter, RBS1 and a low copy *E. coli* replicon, is depicted schematically in Figure 3A. The nucleotide sequence of plasmid pAN004 is set forth as SEQ ID NO:93. pAN006 containing the P_{26} promoter, RBS2 and a medium copy *E. coli* replicon, is depicted schematically in Figure 3B. The nucleotide sequence of plasmid pAN006 is set
- 15 forth as SEQ ID NO:94. The nucleotide sequence of *panBCD* is set forth as SEQ ID NO:59 and the predicted amino acid sequences of PanB, PanC and PanD are set forth as SEQ ID NO:24, SEQ ID NO:26 and SEQ ID NO:28, respectively. Methods for manipulating *Bacilli* are described, for example, in Harwood, C.R. and Cutting, S.M. (editors), *Molecular Biological Methods for Bacillus* (1990) John Wiley & Sons, Ltd.,
- 20 Chichester, England, the content of which is incorporated herein by reference.

EXAMPLE II: Enhanced Production of a Panto-Compound Using Bacteria Overexpressing the *panE1* Gene Product – Ketopantoate Reductase.

This Example describes the cloning of the *B. subtilis panE1* gene and the generation of microorganisms overexpressing the *panE1* gene product.

- 5 Pan⁻ *B. subtilis* strains (e.g., *B. subtilis* mutants blocked in the synthesis of pantothenic acid) had previously been isolated, one of which was reported to be affected in ketopantoate reductase activity (Baigori *et al.* (1991) *J. Bacteriol.* 173:4240-4242). However, the mutations in these strains were incorrectly mapped to the *purE-tre* interval of the *B. subtilis* genetic map which does not contain the *panE* or *panBCD* genes.
- 10 Furthermore as shown below, a *panE* mutant does not have a Pan⁻ phenotype as the *ilvC* gene product can substitute for the *panE* gene product in *B. subtilis* as in other bacterial strains such as *E. coli*. More recently, the *S. typhimurium panE* gene has been located and determined to be allelic to *apbA*, a gene required for anaerobic purine biosynthesis (Frodyma *et al.* (1998) *J. Biol. Chem.* 273:5572-5576). *E. coli* carries a highly
- 15 homologous gene at the same map location. Identification of the *panE* genes in *E. coli* and *S. typhimurium* was complicated by the fact that the *ilvC* gene product, acetohydroxy acid isomeroreductase, is also capable of carrying out the ketopantoate reductase reaction. As a result, pantothenate auxotrophy is not obtained unless both *panE* and *ilvC* are mutated.
- 20 To identify the *B. subtilis panE1* gene, the *B. subtilis* genome was searched using the protein sequence of *E. coli* or *S. typhimurium* ApbA (PanE), and two open reading frames were identified having homology to ApbA, named *ylbQ* and *ykpB*. These genes were renamed *panE1* and *panE2*, due to their proposed function in pantothenate biosynthesis. Both *panE1* and *panE2* were cloned as PCR products generated from
- 25 RL-1 genomic DNA as a template. Both genes were disrupted by either a spectinomycin resistance gene (*spec*) or a chloramphenicol resistance gene (*cat*). The interrupted genes were each integrated by double crossover into PY79 to give PA240 ($\Delta panE1::spec$) and PA241 ($\Delta panE2::cat$). Neither of these strains were pantothenate auxotrophs when tested on pantothenate-free (PF) plates, although PA240 containing
- 30 $\Delta panE1::spec$ grew slightly more slowly on TBAB without added pantothenate than with a 1 mM pantothenate supplement. By comparison, a $\Delta panB::spec$ strain does not produce single colonies on TBAB, presumably because *B. subtilis* has no active uptake system for pantothenate.

- It was hypothesized that the *B. subtilis* gene, *ilvC*, could function for *panE* as had
- 35 been shown for *E. coli*. Accordingly, the *panE1* and *panE2* disruptions were introduced into a strain, CU550, which is reported to be *trpC2 ilvC4 leuC124*. Both the single

panE1 and the double *panE1*, *panE2* disruptants were pantothenate auxotrophs on PF medium.

5 Table 3. Phenotypes of various *panE1* and *panE2* mutants on rich and defined media.

Strain	Medium	Growth*:	
		- pan	+ pan
PY79	TBAB	+++	+++
	PF	++	++
PA240	TBAB spec	+	+++
	PF	++	++
PA241	TBAB cam	+++	+++
	PF	++	++
CU550	TBAB	+++	+++
	PF	++	++
PA256	TBAB spec	-	+++
	PF	-	++
PA258	TBAB spec, cam	-	+++
	PF	-	++

*Each "+" represents about 1 mm of colony diameter after overnight at 37°C.

Thus, mutating both *panE1* and *ilvC* results in pantothenate auxotrophy, while mutating only *panE1* does not, similar to what has been reported for *E.coli* and *S. typhimurium*.

10 Next, the quantitative effect of *panE1* and *panE2* knockouts in a pantothenate overproducing strain (PA235 described herein) was examined. The *panE1* and *panE2* disruptions were introduced into PA235, either singly or together to produce PA245 ($\Delta panE1::spec$), PA248 ($\Delta panE2::cat$) and PA244 ($\Delta panE1::cat$, $\Delta panE2::spec$). The
15 effect of each mutation on pantothenate production was then tested in liquid test tube cultures.

Table 4. *Pantothenate production by PA235 derivatives containing panE1 and panE2 disruptions.*

Strain	[pan] mg/L	% of PA235
PA235	990	(100)
PA235	940	95
PA245	59	6
PA245	82	8
PA248	1060	106
PA248	1030	104
PA244	25	3
PA244	50	5

Thus, deletion analysis indicated that the *panE1* gene contributes to over 90% of the pantothenate production, while deletion of *panE2* did not have a significant effect on pantothenate production. It is therefore concluded that *panE1* accounts for most, but not necessarily all, of the ketopantoate reductase activity in *B. subtilis*. The rest of the ketopantoate reductase activity is predicted to be supplied by *ilvC*.

Having identified *panE1* as an important gene for pantothenate production, increased *panE1* expression was tested to determine whether it could enhance pantothenate production in strains such as PA221 or PA235. The *panE1* coding sequence was installed downstream of the P_{26} promoter and RBS2 in a vector, pOTP61, designed to integrate and amplify at either the *bpr* locus (a non-essential protease gene) or at the locus of the cloned insert. The resulting plasmid, pAN236 (Figure 4) was transformed into PA221, selecting for resistance to tetracycline at 15 mg/L. The nucleotide sequence of pAN236 is set forth as SEQ ID NO:77. One transformant, named PA236 was chosen for further study.

PA236 was shown to overexpress a protein of about 31,000 daltons, which is close to the expected molecular weight of 33,290 daltons for *panE1* protein. Briefly, whole cell extracts were prepared from PY79, RL-1, PA221, PA221/pOTP61 and PA236 (2 samples). Cell extracts were separated by gel electrophoresis and the gels were coomassie stained to visualize proteins. In cells engineered to overexpress *panE* (PA236-1 and PA236-2), a band was visible having an approximate molecular weight of ~31,000 daltons (as compared to molecular weight markers). Moreover, PA221 and PA236 expressed increased levels of a ~29,000 dalton band, corresponding to the *panB*

gene product, and a ~39,000 dalton band, presumably corresponding the *panC* gene product. Furthermore, *E. coli* transformed with pAN006 (Figure 3B) expressed bands correlating to the *panB* and *panC* gene products and *E. coli* transfected with PAN236 expressed a ~31,000 dalton band corresponding to the *panE* gene product.

- 5 Next, PA236 was compared to PA221 carrying the empty vector pOTP61 for pantothenate production in liquid test tube cultures supplemented with 5 g/L β -alanine and 5 g/L α -KIV.

10 **Table 5. Effect of overexpression of *panE1* and *panE2* on pantothenate production by engineered strains in liquid test tube cultures.**

Strain	Additional Plasmid	Gene Overexpressed	[Pantothenate] mg/L
PA221	pOTP61	none	1,000
			940
PA236	pAN236	<i>panE1</i>	2,030
			2,050
PA238	pAN238	<i>panE2</i>	530
			680

- 15 Overexpression of *panE1* caused a two-fold increase in pantothenate production when compared to the parent strain (*e.g.*, to slightly over 2 g/L) whereas overexpression of *panE2* resulted in a strain that produced about 35% less pantothenate than the parent strain. The *panE1* nucleotide sequence and predicted amino acid sequence are set forth as SEQ ID NO:29 and SEQ ID NO:30.

EXAMPLE III: Enhanced Production of a Panto-Compound by Culturing Bacteria Overexpressing *panE1* or *panBCD* in the Presence of Valine.

- 20 The ability of valine to function as a media supplement (*e.g.*, as a substitute for α -KIV) in strains engineered to overexpress the *panBCD* operon and *panE1* was evaluated. Valine is closely related to α -KIV by transamination, is less expensive than α -KIV, and is commercially available in kilogram quantities. Valine was substituted for α -KIV in the standard liquid test tube cultures in SVY medium. The concentration of
- 25 valine was varied from 5 to 50 g/L. Although valine at 5 g/L was slightly less effective

than α -KIV in promoting pantothenate production, valine at 10 or 20 g/L equaled or surpassed 5 g/L α -KIV in promoting pantothenate production.

5 **EXAMPLES IV-X Generation of Microorganisms Capable of Producing Pantothenate in a Precursor-Independent Manner**

B. subtilis strains such as PA221 and PA235 (engineered to overexpress *panBCD*) and PA236 (engineered to overexpress *panBCD* and *panEI*) need to be fed α -ketoisovalerate (α -KIV) (or valine) and aspartate (or β -alanine) to achieve maximal pantothenate production, as both these precursors are limiting for pantothenate
10 synthesis. Accordingly, manipulated microorganisms were designed to eliminate the need to feed limiting precursors of pantothenate biosynthesis in the production of pantothenate. These strains are also useful in the production of various pantothenate biosynthetic pathway intermediates.

15 **EXAMPLE IV: Generation of Microorganisms Capable of Producing Pantothenate in an Aspartate- (or β -Alanine) Independent Manner**

The *panD* gene was cloned into *B. subtilis* expression vector pOTP61 to construct pAN423 (Figure 5). The nucleotide sequence of pAN423 is set forth as SEQ ID NO:78. The *NotI* restriction fragment containing *panD* was isolated from pAN423,
20 self ligated and used to transform PA221. Transformants resistant to Tet¹⁵, Tet³⁰, and Tet⁶⁰ were isolated and saved for further analysis.

Six of the pAN423 transformants plus two control transformants were grown in SVY containing 5 g/l α -KIV with and without 10 g/l aspartate and then assayed for pantothenate production (Table 6).

25

Table 6. Effect of overproducing PanD on pantothenate production with and without added aspartate.

Culture* (PA221 transformants)	Asp (10 g/L)	TetR** (μ g/ml)	OD550	[pan] (mg/L)
pOTP61-1	-	60	8.0	76
pOTP61-2	-	60	7.7	91
423#1-1	-	15	8.5	180
423#1-2	-	15	8.0	150
423#1-3	-	30	8.3	220
423#1-4	-	30	8.5	280
423#1-5	-	60	8.9	580
423#1-6	-	60	8.8	280

pOTP61-1	+	60	7.5	380
pOTP61-2	+	60	6.9	560
423#1-1	+	15	8.5	1200
423#1-2	+	15	8.6	1000
423#1-3	+	30	8.8	1200
423#1-4	+	30	9.0	1200
423#1-5	+	60	9.0	1200
423#1-6	+	60	9.0	1200

*Test tubes cultures were grown in SVY + α -KIV (5 g/L) with Asp (10 g/L) where indicated.

**TetR = Approximate Tet-resistance of transformant

The pAN423 transformants produced at least twice the amount of pantothenate as the controls (*i.e.*, to a level at or near that which was obtained in earlier experiments by the addition of β -alanine to the culture medium). The data also show that in the absence of added aspartate, transformants containing additional copies of the *panD* gene expression cassette produce more pantothenate than the control transformants. One of the transformants, 423#1-5, produced about five times as much pantothenate as the controls. These results indicated that increased levels of PanD protein "pull" the conversion of available aspartate towards β -alanine, and that increasing *panD* gene expression can result in enhancement of pantothenate production both in the presence and absence of added aspartate.

Transformant 423#1-5 was re-named strain PA401 and studied further in shake flask fermentations. The shake flask medium was SVY with maltose instead of SVY with glucose. Results of shake flask experiments agreed well with test tube experiments during the first 24 hours. In shake flask experiments without the addition of β -alanine, PA401 produced approximately 1.5 g/l of pantothenate in 24 hours. Addition of β -alanine to the culture medium did not further improve pantothenate titers (Table 7), indicating that with this strain and these fermentation conditions, β -alanine is not limiting pantothenate production. In fact, when no β -alanine is fed, one can observe that PA401 is secreting β -alanine in significant amounts into the medium.

Table 7. Shake flask cultures with strain PA401 (*panD*) with and without β -alanine.

Initial β -ala Added	Amino acids (g/l)		24 hours		
	β -ala	Val	pH	OD ₆₀₀	Pantothenate (g/l)
0	0.7	1.5	7.5	13.7	1.5
5 g/l	7.1	1.4	7.6	12.4	1.5

Each value represents the average of duplicate 250 ml baffled flasks containing 50 ml of medium, incubated at 37°C with shaking (200 rpm).

Base Medium: SVY with 10 g/l α -KIV, 30 g/l maltose

2% Inoculum: SVY with Tet^r grown 24 hours.

EXAMPLE V: Engineering the *panD* gene for Further Increased Synthesis of Aspartate Decarboxylase and Enhanced Production of Pantothenate

This Example describes the generation of improved ribosome binding sites (RBSs) in the *panD* gene to increase the translation of *panD* mRNA.

Increasing the translation of the *panD* gene mRNA by generation of synthetic *panD* RBSs

- The RBS (SEQ ID NO:88) used to express *panD* in pAN423 is a synthetic RBS and has been used to successfully produce other proteins in *B. subtilis* at a high level. However, it contains six mismatches when aligned to the "ideal" *B. subtilis* RBS (SEQ ID NO:45) (e.g., an RBS having a sequence which is complementary to the 16S RNA sequence within the *B. subtilis* ribosome). (See e.g., Table 1B, mismatches in bold).
- Two new RBSs were designed to more closely mimic the ideal RBS. These synthetic RBSs, named new design A (NDA) and new design B (NDB) (also referred to herein as RBS3 and RBS4), are set forth as SEQ ID NO:51 and SEQ ID NO:52 and are aligned with the ideal RBS in Table 1B.

- Oligonucleotides corresponding to the top and bottom strands of each new RBS were synthesized, annealed, then used to replace the RBS in pAN420, generating plasmids pAN426 and pAN427. These constructions are illustrated in Figure 6. The presence of the NDA and NDB RBS in pAN426 and pAN427 was confirmed by DNA sequence analysis. Next, the *panD* genes from pAN426 and pAN427 were transferred to *B. subtilis* expression vector pOTP61 as shown in Figure 7, creating pAN428 and pAN429. The nucleotide sequence of pAN429 is set forth as SEQ ID NO:79.

NotI restriction fragments lacking the *E. coli* vector sequences were isolated from pAN428 and pAN429, self-ligated, and used to transform strain PA221 to resistance to Tet¹⁵. Four isolates resistant to Tet⁶⁰ were picked from each transformation and assayed for pantothenate and β -alanine production along with PA221 transformed with the empty vector (pOTP61) and PA221 transformed with pAN423 (strain PA401) (see Table 8).

Table 8. *Panthothenate production by test tube cultures of PA221 transformed with pAN428 and pAN429*

Plasmid	Medium Supplements	OD550	Pan g/l	β -Ala g/l
pOTP61	α -KIV ⁵	10	UND	0.04
pAN423	α -KIV ⁵	10	0.4	0.04
pAN428-1 *	α -KIV ⁵	12	0.6	0.04
pAN428-2	α -KIV ⁵	11	0.5	0.03
pAN428-3	α -KIV ⁵	11	0.3	0.03
pAN428-4	α -KIV ⁵	10	0.1	UND
pAN429-1	α -KIV ⁵	12	0.6	0.04
pAN429-2	α -KIV ⁵	11	0.5	0.04
pAN429-3	α -KIV ⁵	11	0.6	0.05
pAN429-4 #	α -KIV ⁵	12	0.8	0.10
pOTP61	α -KIV ⁵ + Asp ¹⁰	11	0.5	0.08
pAN423	α -KIV ⁵ + Asp ¹⁰	12	0.9	1.32
pAN428-1 *	α -KIV ⁵ + Asp ¹⁰	12	0.8	1.97
pAN428-2	α -KIV ⁵ + Asp ¹⁰	12	0.8	1.51
pAN428-3	α -KIV ⁵ + Asp ¹⁰	12	0.9	1.02
pAN428-4	α -KIV ⁵ + Asp ¹⁰	11	0.8	0.30
pAN429-1	α -KIV ⁵ + Asp ¹⁰	12	0.8	1.78
pAN429-2	α -KIV ⁵ + Asp ¹⁰	12	0.8	1.66
pAN429-3	α -KIV ⁵ + Asp ¹⁰	12	0.8	1.78
pAN429-4 #	α -KIV ⁵ + Asp ¹⁰	13	0.8	2.28

UND: Below the limits of detection. * Renamed PA402 # Renamed PA403

When grown in medium supplemented with α -KIV at 5 g/l (α -KIV⁵), the pAN428-1 transformant and all four of the pAN429 transformants produced more

pantothenate than did PA401, suggesting that these transformants contain higher levels of aspartate decarboxylase activity. When grown in medium supplemented with α -KIV⁵ and Asp¹⁰ none of the pAN428 or pAN429 transformants produced more pantothenate than PA401. However, the pAN428-1 transformant and all four of the pAN429 transformants produced significantly more β -alanine than did PA401. It is possible that the excess β -alanine produced from added aspartate causes inhibition of pantothenate production. Alternatively, β -alanine may accumulate because pantoate is limiting in these strains.

The strains that produced the highest level of β -alanine, the pAN428-1 and pAN429-4 transformants, were renamed PA402 and PA403, respectively. These two strains were grown in SVY medium supplemented with various intermediates and reassayed for pantothenate and β -alanine production. PA221 and PA401 were included as controls. The results of the assays are presented in Table 9.

Table 9. Pantothenate production of PA402 and PA403 in test tube cultures.

Strain	Medium Supplements	OD550	Pan g/l	β -Ala g/l	Val g/l
PA221	α -KIV ⁵	7.9	UND	UND	0.9
PA401	α -KIV ⁵	8.7	0.3	0.04	0.9
PA402	α -KIV ⁵	8.5	0.5	0.04	0.9
PA403	α -KIV ⁵	9.4	0.7	0.07	0.9
PA221	α -KIV ⁵ + Asp ¹⁰	9.8	0.4	0.11	0.8
PA401	α -KIV ⁵ + Asp ¹⁰	9.1	0.8	1.15	0.8
PA402	α -KIV ⁵ + Asp ¹⁰	9.4	0.8	2.02	0.8
PA403	α -KIV ⁵ + Asp ¹⁰	9.7	0.7	2.40	0.8
PA221	Pantoate ⁵	8.9	UND	UND	0.2
PA401	Pantoate ⁵	8.7	0.3	0.02	0.2
PA402	Pantoate ⁵	10.6	0.5	0.02	0.2
PA403	Pantoate ⁵	10.5	0.7	0.02	0.2
PA221	Pantoate ⁵ + Asp ¹⁰	9.5	0.4	0.06	0.2
PA401	Pantoate ⁵ + Asp ¹⁰	9.2	2.2	0.62	0.2
PA402	Pantoate ⁵ + Asp ¹⁰	9.1	2.8	1.17	0.2
PA403	Pantoate ⁵ + Asp ¹⁰	10.2	2.9	1.58	0.2

UND: Below the limits of detection.

When grown in medium supplemented with either α -KIV⁵ or Pantoate⁵, PA402 and PA403 produced significantly more pantothenate than did PA401. As before, even though PA402 and PA403 produced significantly more β -alanine than PA401 when
5 grown in medium supplemented with α -KIV⁵ and Asp¹⁰, they did not produce a proportional increase in pantothenate. However, when grown in medium supplemented with Pantoate⁵ plus Asp¹⁰, both PA402 and PA403 produced significantly more pantothenate than PA401, about a 30% increase.

It can be concluded from these experiments that the improved NDA and NDB
10 *panD* ribosome binding sites, engineered into pAN428 and pAN429, respectively, lead to increased levels of aspartate decarboxylase activity.

Increasing the translation of the *panD* gene mRNA by generation of synthetic *panD*
RBSs within the *panBCD* operon

15

The native *B. subtilis panD* gene ribosome binding site (RBS) (SEQ ID NO:43), which is found in the *P₂₆panBCD* operon cassette present in PA221 (and in other engineered pantothenate production strains described herein), is shown in Table 1C aligned with the ideal ribosome binding site (SEQ ID NO:47). The alignment shows
20 mismatches between the native *B. subtilis panD* gene RBS, which is located within the coding sequence for PanC, and the the ideal RBS. Three new RBSs (within the P26 *panBCD* operon cassette) were generated to increase translation of the *panD* gene mRNA and to yield increased synthesis of aspartate decarboxylase. These synthetic RBSs (termed NDI, NDII, and NDIII, also referred to herein as RBS5, RBS6 and RBS7,
25 respectively) are set forth as SEQ ID NO:55, SEQ ID NO:56 and SEQ ID NO:57, respectively) and are included in Table 1C. It should be noted that although changes in the *panD* RBS within the *panBCD* operon also changes the C-terminal amino acid sequence of the PanC protein encoded by that operon, an alignment of known and suspected PanC protein amino acid sequences showed that the sequence of the last nine
30 amino acids of the *B. subtilis* PanC protein could be altered without affecting any conserved amino acid residues indicating that such changes should not reduce pantothenate synthetase activity or expression. The new RBSs were synthesized and incorporated into the *P₂₆panBCD* operon expression cassette as follows.

First, PCR primers were designed to contain the following elements: (1) a
35 nucleic acid sequence encoding the first five amino acids of PanD up to and including a unique *Bsi*WI restriction site that had been previously introduced into *panD* by PCR; (2)

a stop codon for *panC*, (3) at least one synthetic RBS; and (4) 30-39 bp of nucleic acid sequence having 100% identity with *panC* upstream of the *panD* RBS. The primers were named TP102, TP103, and TP104 and contain the NDI, NDII, and NDIII ribosome binding sites, respectively. These three primers were used in conjunction with the 5' primer TP101, which hybridizes near the start codon of *panC*, in three independent PCR reactions to generate the NDI, NDII, and NDIII PCR products. The PCR products were purified, digested with *XbaI*, then cloned into plasmid vector pASK-1BA3 which had been digested with *XbaI* and *SmaI*. The resulting plasmids were named pAN431, pAN432, and pAN433. The construction of pAN431 is illustrated in Figure 8 and is representative of all three plasmid constructions. The presence of the desired synthetic *panD* gene RBS in each new plasmid was confirmed by DNA sequencing.

Next, the modified *panC* genes containing the new *panD* RBSs were joined with the *panD* gene utilizing the unique *BsiWI* restriction site. This was accomplished by isolating the appropriate *NsiI-BsiWI* restriction fragments from pAN431, pAN432, and pAN433 and ligating them with a 2395 bp *NsiI-BsiWI* restriction fragment from pAN420, which supplied the *BsiWI*-modified *panD* gene. These constructions resulted in plasmids pAN441, pAN442, and pAN443, respectively. A representative construction (pAN441) is illustrated in Figure 9. The nucleotide sequence of pAN443 is set forth as SEQ ID NO:80.

The new *panD* gene RBSs were then substituted into the $P_{26}panBCD$ operon expression cassette as follows. First, a deletion-insertion mutation which removes the region of *panC* containing the *panD* RBS was created. This was constructed by digesting pAN430 with a mixture of *BspEI* and *BglII* and recovering the 4235 bp fragment which is now missing the 3' end of *panC* and the 5' end of *panD*. This fragment was ligated with an *AvaI-BamHI* restriction fragment from plasmid pECC4, which contains the chloramphenicol acetyl transferase (*cat*) gene. The 5' extension produced by *AvaI* digestion is compatible with that produced by *BspEI* while the *BglII* and *BamHI* extensions are also compatible. The resulting plasmid was named pAN440, and its construction is illustrated in Figure 10.

The resulting deletion-insertion mutation was crossed into the $P_{26}panBCD$ operon *via* homologous recombination by transforming PA221 with linearized pAN440 and selecting for resistance to chloramphenicol on Cam^S plates containing 1 mM pantothenate. Several transformants were tested, and were all found to require 1 mM pantothenate for growth, as expected. Two of these transformants were remaned PA408A and PA408B and were assayed for pantothenate production. Neither strain synthesized measurable quantities of pantothenate, even when grown in medium

containing pantoate and β -alanine at 5 g/l, indicating that the strains are deficient in pantothenate synthetase activity. Next, the new *panD* RBSs were crossed into the *P*₂₆ *panBCD* operon by transforming PA408 with linearized pAN441, pAN442, and pAN443 plasmid DNA and selecting for growth on TBAB plates without pantothenate supplementation. A transformation with linearized pAN430 (including the native *panD* RBS) was included as a control and was expected to give rise to transformants identical to PA221 described herein. Four isolates from each transformation were assayed for pantothenate and β -alanine production in SVY medium supplemented with various intermediates (Tables 10 and 11).

Table 10. Pantothenate production of PA410 - PA413 in test tube cultures.

Strain	RBS	Medium Supplements	OD550	Pan g/l	β -Ala g/l
PA221	native	Pantoate ⁵	11	UND	UND
PA410-1	native	Pantoate ⁵	12	UND	UND
PA410-2		Pantoate ⁵	12	UND	UND
PA410-3		Pantoate ⁵	12	UND	UND
PA410-4		Pantoate ⁵	12	UND	UND
PA411-1	NDI	Pantoate ⁵	12	0.23	UND
PA411-2		Pantoate ⁵	12	0.20	UND
PA411-3		Pantoate ⁵	12	0.19	UND
PA411-4		Pantoate ⁵	12	UND	UND
PA412-1	NDII	Pantoate ⁵	12	UND	UND
PA412-2		Pantoate ⁵	11	UND	UND
PA412-3		Pantoate ⁵	13	0.18	UND
PA412-4		Pantoate ⁵	12	0.18	UND
PA413-1	NDIII	Pantoate ⁵	12	0.18	UND
PA413-2		Pantoate ⁵	12	0.17	UND
PA413-3		Pantoate ⁵	12	0.16	UND
PA413-4		Pantoate ⁵	12	0.17	UND

UND: Below the limits of detection.

Table 11. Pantothenate production of PA410 - PA413 in test tube cultures.

Strain	RBS	Medium Supplements	OD550	Pan g/l	β -Ala g/l
PA221	native	Pantoate ⁵ + Asp ¹⁰	11	0.3	UND
PA410-1	native	Pantoate ⁵ + Asp ¹⁰	12	0.4	UND
PA410-2		Pantoate ⁵ + Asp ¹⁰	12	0.4	UND
PA410-3		Pantoate ⁵ + Asp ¹⁰	12	0.4	UND
PA410-4		Pantoate ⁵ + Asp ¹⁰	12	0.4	UND
PA411-1	NDI	Pantoate ⁵ + Asp ¹⁰	13	1.7	0.4
PA411-2		Pantoate ⁵ + Asp ¹⁰	13	1.7	0.4
PA411-3		Pantoate ⁵ + Asp ¹⁰	13	1.8	0.3
PA411-4		Pantoate ⁵ + Asp ¹⁰	13	0.4	UND
PA412-1	NDII	Pantoate ⁵ + Asp ¹⁰	13	0.4	UND
PA412-2		Pantoate ⁵ + Asp ¹⁰	12	0.4	UND
PA412-3		Pantoate ⁵ + Asp ¹⁰	12	1.6	0.3
PA412-4		Pantoate ⁵ + Asp ¹⁰	12	1.5	0.2
PA413-1	NDIII	Pantoate ⁵ + Asp ¹⁰	13	1.6	0.3
PA413-2		Pantoate ⁵ + Asp ¹⁰	13	1.6	0.4
PA413-3		Pantoate ⁵ + Asp ¹⁰	13	1.7	0.4
PA413-4		Pantoate ⁵ + Asp ¹⁰	13	1.7	0.4

UND: Below the limits of detection.

- 5 As expected from previous experiments using PA221, none of the transformants that contained the native *panD* RBS produced measurable quantities of pantothenate when grown in medium supplemented with pantoate. However, nine of the twelve transformants expected to contain modified *panD* RBSs produced significant quantities of pantothenate (160-230 mg/l) under these conditions, indicating that they possess
- 10 elevated levels of aspartate decarboxylase activity. When grown in medium supplemented with both pantoate and aspartate, these same nine transformants produced approximately four times more pantothenate than those with the native *panD* RBS. In addition, these nine transformants accumulated measurable quantities of β -alanine (230-410 mg/l). All transformants produced roughly equivalent quantities of pantothenate
- 15 when grown in medium containing pantoate and β -alanine, demonstrating that each contains a functional pantothenate synthetase.

These data demonstrate that the synthetic *panD* RBSs are about four times more effective than the native *panD* RBS in directing translation of the *panD* gene mRNA and evidence the utility of such synthetic RBSs in enhancing pantothenate production.

Additional approaches to increasing pantothenate production can include, for example, increasing the half-life of the *panD* gene mRNA, increasing the strength of the promoter for *panD* transcription and/or increasing the stability of the PanD protein.

EXAMPLE VI: Construction of Strains Containing an Integrated P_{26} *panE1* Cassette without an Antibiotic Resistance Gene.

Example II describes the identification of the *B. subtilis* *panE1* gene that encodes the enzyme responsible for the majority of the ketopantoate reductase activity in *B. subtilis*. PA236 (containing the pAN236 plasmid) produced about twice as much pantothenate (2 g/l) as its parent strain, PA221 (1 g/l) in 24 hour SVY test tube cultures. PA236 was presumed to contain an amplified (~3 copies) integrated pAN236 plasmid based on selection for tetracycline resistance (the *tetR* gene product being encoded on the pAN236 plasmid in addition to the P_{26} *panE1* cassette). Also useful in the methodologies of the present invention are strains that contain a single integrated unamplifiable copy of P_{26} *panE1* at the *panE1* locus, for example, without an antibiotic resistance gene in the strain. Such a strain was generated as follows.

A plasmid named pAN251 was derived from pAN236 by inserting additional chromosomal sequences just upstream and just downstream from the P_{26} *panE1* cassette. These additional sequences, which provide homology to allow integration of the P_{26} *panE1* cassette at *panE1* by double crossover, were obtained by PCR from chromosomal DNA as a template. pAN251 is shown in Figure 11. The nucleotide sequence of pAN251 is set forth as SEQ ID NO:81.

Next, a strain was constructed which allowed selection for the incoming P_{26} *panE1* cassette. The strain included the following three components: (1) P_{26} *panBCD*; (2) Δ *panE1*; and (3) *ilvC*, since both *panE1* and *ilvC* must be mutated to have a Pan⁻ phenotype. The starting strain was CU550 (*trpC2*, *ilvC4*, *leuC124*). The P_{26} *panBCD* cassette from PA221 chromosomal DNA was introduced in two steps to create strain PA290. Next, Δ *panE1*::*spec* was transformed into PA290, using chromosomal DNA from strain PA240, to give strain PA294 (*trpC2*, *ilvC4*, *leuC124*, P_{26} *panBCD*, Δ *panE1*::*spec*), which is a strict pantothenate auxotroph. Finally, PA294 was transformed with plasmid pAN251, selecting for pantothenate prototrophy, to give strain PA303. This strain was expected to have the genotype *trpC2*, *ilvC4*, *leuC124*, P_{26}

panBCD, P_{26} *panE1*. PA303 was checked for the correct chromosomal structure at the *panE1* locus by PCR using primers that flank the P_{26} insertion just upstream of *panE1*. The PCR product from PA303 was of the expected size, with a concomitant loss of the PCR product from the wild type *panE1* gene, consistent with having obtained the
 5 desired double crossover event. Furthermore, PA303 was tetracycline sensitive, which is also consistent with the desired double crossover event, as opposed to a Campbell-type single crossover of the plasmids into the chromosome. The *trp*, *ilv*, and *leu* auxotrophies from the parent strain were all maintained in PA303.

10 In 24 hour liquid SVY test tube cultures, PA303 produced almost the same level of pantothenate as positive control PA236, and about twice as much as PA221, which does not contain engineered *panE1* as indicated in Table 12.

Table 12. Pantothenate production by 24 hr. test tube cultures of PA303 and controls grown in SVY plus 5 g/l α -KIV and 5 g/l β -alanine.

15

Strain	OD ₆₀₀	[pan] g/l
PA221-1	10.9	0.85
PA221-2	10.5	0.85
PA236-1	9.5	1.74
PA236-2	9.3	1.70
PA303-1	10.8	1.66
PA303-2	10.7	1.61

EXAMPLE VII: Generation of Microorganisms Capable of Producing Pantothenate in an α -KIV (or Valine) Independent Manner

20 α -ketoisovalerate (α -KIV) is a rate limiting intermediate for pantothenate production in certain strains deregulated for pantothenate synthesis. Addition of either α -KIV or valine at 5 g/l increases pantothenate production about 5-fold in test tube cultures with strains such as PA221. In order to alleviate the need to feed either α -KIV or valine, strains were engineered that have an increased capacity to synthesize α -KIV.

25 α -KIV is produced in *B. subtilis* from pyruvate by the sequential action of three enzymes encoded by four genes, *ilvB* and *ilvN*, *ilvC*, and *ilvD*. In a wild type *B. subtilis*, three of the genes (*ilvB*, *ilvN*, and *ilvC*) are the first three genes of the large *ilv-leu* operon. The fourth gene necessary for α -KIV synthesis, *ilvD*, is located by itself elsewhere on the chromosome. The *B. subtilis* *ilv-leu* operon is thought to be regulated

only by leucine levels. Feeding of exogenous leucine reduces transcription of the *ilv-leu* operon by about 13-fold, probably by an attenuation mechanism (Grandoni *et al.* (1992) *J. Bacteriol.* 174: 3212-3219). The only known feedback regulation in the *ilv-leu* pathway is the inhibition of the *leuA* gene product by leucine.

- 5 As a first step to deregulate the synthesis of α -KIV, a copy of the *ilvBNC* region from the wild type *B. subtilis* *ilv-leu* operon was isolated by PCR, and installed adjacent to the P_{26} promoter and RBS2 on a vector, pOLL8, that was designed to integrate a single P_{26} expression cassette by double recombination at the *amyE* locus. The *amyE* gene encodes a nonessential α -amylase, and is a useful locus for installing expression
10 cassettes. The resulting plasmid, pAN267, is illustrated in Figure 12. The nucleotide sequence of pAN267 is set forth as SEQ ID NO:82. pAN267 readily gave stable transformants by double crossover at the *amyE* locus of *B. subtilis* strains, as described in detail below.

Construction of pantothenate overproducing strains that are leucine prototrophs

- 15 Initially, a *B. subtilis* strain containing *ilvC4* and Δ *panE1* was used to introduce a single copy of P_{26} *panE1* into the chromosome without using an antibiotic resistance gene. The double mutant was required to select for the incoming P_{26} *panE1* cassette because a Δ *panE1* mutation alone does not result in pantothenate auxotrophy. A strain named CU550 was obtained containing *ilvC4* to be used as a basis for this type of strain
20 construction. However, CU550 also contains a closely linked *leuC124* mutation, so all strains derived from CU550 required leucine. Having shown that the combination of P_{26} *panBCD* and P_{26} *panE1* was favorable for pantothenate production, the next step was to reassemble this combination of two cassettes in a leucine prototroph.

- Accordingly, the two cassettes were combined in two different strain
25 backgrounds, RL-1 and PY79. To introduce chromosomal P_{26} *panE1* into the PY79 and RL-1 strain backgrounds without using an antibiotic resistance gene, a strategy was used that did not rely on *ilvC4*. (The strategy took advantage of the observation that the Δ *panE1* mutation causes a pantothenate bradytroph, manifested by relatively small colonies on TBAB (rich) plates). First, Δ *panB::cat* and Δ *panE::spec* were introduced
30 into both strain backgrounds. Next, the resulting strains were transformed simultaneously with DNA from two strains, PA221 (P_{26} *panBCD*) and PA303 (P_{26} *panE1*), selecting for Pan⁺ on TBAB plates. Colonies of two distinct sizes grew on the selective plates, with the larger size comprising about 2% of the colonies. The larger colonies were presumed to represented co-transformants that received both P_{26} *panBCD*
35 and P_{26} *panE1*, and that the smaller colonies had received only P_{26} *panBCD*. Consistent

with this prediction, the larger colonies had lost both *Cam^r* and *Spec^r*, while the smaller colonies had lost only the *cat* gene, and retained the *spec* gene. Furthermore, a representative derivative of PY79 named PA327, and a representative derivative of RL-1, named PA328, both produced the elevated levels of pantothenate in test tube cultures which was about 1.6 to 1.7 g/l (Table 13).

Table 13. *Pantothenate production of PA327, PA328, and controls from 24 hr test tube cultures grown in SVY plus 5 g/l α -KIV and β -alanine.*

Strain	Background	<i>P</i> ₂₆ <i>panE1</i> copy number	[pan] g/l
PA221-1	RL-1	0	0.92
PA221-2	RL-1	0	0.95
PA236-1	RL-1	amplified (~3)	1.60
PA236-2	RL-1	amplified (~3)	1.73
PA327-1	PY79	1	1.66
PA327-2	PY79	1	1.65
PA328-1	RL-1	1	1.61
PA328-2	RL-1	1	1.91

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Thus, PA327 and PA328 were concluded to contain both *P*₂₆ *panBCD* and *P*₂₆ *panE1*, and were used for further constructions as described below. PCR analysis confirmed the presence of the two cassettes.

15 Installation of a stable *P*₂₆ *ilvBNC* cassette into two lineages of pantothenate overproducing strains

Having constructed PA327 and PA328, derivatives of PY79 and RL-1 that contain *P*₂₆ *panBCD* and *P*₂₆ *panE1*, and that are *Leu⁺*, the next step was to introduce stable copies of *P*₂₆ *ilvBNC*. This was accomplished by transforming PA327 and PA328 with plasmid pAN267, selecting for *Spec^r*. Screening by PCR showed that about 85% of the obtained transformants contain *P*₂₆ *ilvBNC* integrated at *amyE* by double crossover. One transformant of PA327, named PA340, and one transformant of PA328, named PA342, were chosen for further study.

In test tube cultures grown in SVY medium plus 5 g/l β -alanine but without added α -KIV, both PA340 and PA342 gave the expected increase in pantothenate production over that of PA327 and PA328, to about 1.3 to 2 g/l (Table 14).

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Table 14. *Pantothenate and valine production by PA340 and PA342, both containing P₂₆ ilvBNC in 24 hr test tube cultures grown in SVY with 5 g/l β -alanine and with or without 5 g/l α -KIV*

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Strain	Back-ground	OD ₆₀₀		[pan] g/l		[val] g/l	
		- α -KIV	+ α -KIV	- α -KIV	+ α -KIV	- α -KIV	+ α -KIV
PA340-1	PY79	11.8	7.1	2.02	2.10	0.38	0.90
PA340-2	PY79	10.3	7.5	1.97	2.03	0.40	0.91
PA342-1	RL-1	10.2	8.0	1.29	1.89	0.27	0.78
PA342-2	RL-1	9.6	9.2	1.34	2.04	0.21	0.79

The two new strains also gave a slight increase in valine secretion, indicating that the *ilvBNC* genes had been deregulated. However, when the same strains were grown with 5 g/l α -KIV added, a further increase in pantothenate production occurred from PA342, suggesting that α -KIV was still rate limiting in this strain background. Similar results, only with more growth and hence higher pantothenate levels, were seen in shake flask cultures (Table 15).

Table 15. *Pantothenate and valine production by PA340 and PA342, both containing P₂₆ ilvBNC in 24 hour shake flask cultures grown in SVY with 5 g/l β -alanine and with or without 5 g/l α -KIV.*

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Strain	Back-ground	OD ₆₀₀		[pan] g/l		[val] g/l	
		- α -KIV	+ α -KIV	- α -KIV	+ α -KIV	- α -KIV	+ α -KIV
PA327	PY79	21	22	0.6	3.0	0.5	1.3
PA340-1	PY79	20	20	3.5	4.1	1.0	1.9
PA340-2	PY79	22	19	3.0	2.1	0.8	1.4
PA328	RL-1	20	16	1.4	2.7	0.6	1.3
PA342-1	RL-1	17	16	3.3	3.6	0.9	1.6
PA342-2	RL-1	18	18	3.1	4.2	0.8	1.4

EXAMPLE VIII: Increasing *panD* Copy Number in Strains Engineered to Overproduce *panE1* and the *ilvBNC* Gene Products Enhances Pantothenate Production

Experiments where β -alanine was fed to cultures of engineered *B. subtilis* strains consistently showed that β -alanine was a rate limiting intermediate in pantothenate synthesis. The effect of adding additional copies of *panD* on pantothenate production in PA340 and PA342 was examined. Strains PA340 and PA342 were transformed with chromosomal DNA isolated from PA401 with selection on plates containing 15 μ g/ml of tetracycline (Tet¹⁵ plates). Transformants derived from each parent were patched onto Tet⁶⁰ plates to identify those which were likely to contain multiple copies of the expression cassette. Twelve transformants from each transformation which grew on Tet⁶⁰ were streaked for single colonies on this medium and then assayed in SVY medium test tube cultures for pantothenate production. One transformant from each group was found to produce greater than 300 mg/l pantothenate in 24 hours. These two transformants were saved and named PA404 (PA340 strain background) and PA405 (PA342 strain background). Both strains were resistant to spectinomycin, indicating that the *P₂₆ ilvBNC* expression cassette was still present at *amyE*. PCR analysis of chromosomal DNA isolated from each strain confirmed that the deregulated *panE1* gene had also been retained.

Next, PA404 and PA405 were evaluated in shake flask cultures which were grown in SVY medium containing maltose as the carbon source and supplemented with various intermediates. The cultures were grown for 24 and 48 hours and then assayed for pantothenate, β -alanine, and valine production. The results of this experiment are presented in Table 16. Analogous shake flask culture data for the parent strains (PA340 and PA342) are included in the tables for comparison.

Table 16. Pantothenate production by PA404 and PA405 in shake flask cultures after 24 hours

Strain	Medium Supplements	OD ₆₀₀	Pan g/l	β -Ala g/l	Val g/l
PA340	none	20	0.4	<0.1	1.0
PA404	none	22	1.8	<0.1	0.7
PA342	none	19	0.3	0.2	0.7
PA405	none	19	1.4	0.4	0.5

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PA340	β -alanine ^S	18	3.6	3.2	0.6
PA404	β -alanine ^S	18	2.8	5.1	0.7
PA342*	β -alanine ^S	17	3.3	3.3	0.5
PA405*	β -alanine ^S	19	1.3	6.5	0.6

Values are the average of duplicate flasks except where indicated by *.

In the absence of any medium supplementation, PA404 and PA405 made four to five times more pantothenate in 24 hours compared to their isogenic parent strains (Table 16). The supply of β -alanine was clearly limiting in the parent strains PA340 and PA342. Addition of amplified *P26 panD* greatly increased the supply of β -alanine.

EXAMPLE IX: Deregulation of the *B. subtilis ilvD* Gene Enhances Pantothenate Production

To deregulate expression of the *ilvD* gene, standard procedures (described above) were used to integrate the constitutive *P₂₆* promoter and an artificial ribosome binding site, RBS2, just upstream of the *ilvD* coding region. The *ilvD* gene maps by itself, unlinked to the *ilvBNC* operon. First, a 2.4 kb region of the RL-1 chromosome that contains the *ilvD* coding region and 730 bp of upstream sequence was cloned by PCR into a low copy (about 15 per *E. coli* cell) vector called pOK12, to give plasmid pAN257, shown in Figure 13.

Taking advantage of a natural *EcoRI* site just upstream of the native *ilvD* gene promoter, and a natural *NcoI* site at the *ilvD* start codon, an artificial sequence containing *P₂₆* and RBS2 was inserted into pAN257 to give pAN263 (Figure 14). The nucleotide sequence of pAN263 is set forth as SEQ ID NO:83. In parallel with this construction, the *cat* gene was also inserted into pAN257, between the same upstream *EcoRI* site and a *BglII* site in the middle of the *ilvD* coding region, to give pAN261, which is deleted for a large portion of the *ilvD* gene (Figure 15). Using pAN261 and pAN263, the *P₂₆ ilvD* cassette could then be installed in the *B. subtilis* chromosome in two steps. In the first step, pAN261 is introduced by transformation, selecting for chloramphenicol resistance, and then confirming an *Ilv⁻* phenotype. In the second step, pAN263 is introduced, selecting for *Ilv⁺*, checking for chloramphenicol sensitivity, and confirming correct local structure by PCR.

pAN261 was first transformed into strain RL-1 (highly competent) to give strain PA343 ($\Delta ilvD::cat$), and then chromosomal DNA from PA343 was used to transform PA340 and PA342 to *Ilv⁻* auxotrophy, yielding strains named PA348 and PA349, respectively. Chromosomal DNA is inherently more efficient than monomeric plasmid

in transforming *B. subtilis*. Similarly, pAN263 DNA was transformed into PA343 (moderately competent) to give strain PA345 (P_{26} *ilvD*), and then PA345 chromosomal DNA was used to transform PA348 and PA349 to *Ilv*⁺ prototrophy, yielding strains PA374 and PA354, respectively.

- 5 As predicted, PA374 and PA354 gave further increases in pantothenate production, to about 2.5 to 2.9 g/l, in test tube cultures grown in SVY plus 5 g/l β -alanine (Table 17).

10 Table 17. Pantothenate and valine production by PA374 and PA354, containing P_{26} *ilvD*, and controls, in 24 hr test tube cultures grown in SVY with 5 g/l β -alanine and with or without 5 g/l α -KIV.

Strain	Back-ground	<i>ilvD</i> status	OD ₆₀₀		[pan] g/l		[val] g/l	
			α -KIV -	+	α -KIV -	+	α -KIV -	+
PA340	PY79	w.t.	9.2	9.0	2.14	2.23	0.38	0.90
PA348	PY79	<i>ilvD::cat</i>	11.7	10.0	0.19	2.23	0.19	0.91
PA374-1	PY79	P_{26} <i>ilvD</i>	9.1	7.3	2.93	2.40	0.58	0.87
PA374-2	PY79	P_{26} <i>ilvD</i>	8.2	7.7	2.99	2.36	0.60	0.95
PA342	RL-1	w.t.	10.2	8.0	1.29	1.89	0.27	0.78
PA349	RL-1	<i>ilvD::cat</i>	8.1	7.7	0.17	1.87	0.22	0.88
PA354-1	RL-1	P_{26} <i>ilvD</i>	9.6	9.6	2.57	2.03	0.65	1.23
PA354-2	RL-1	P_{26} <i>ilvD</i>	7.5	8.2	2.48	2.24	0.64	0.97

- 15 In the absence of added β -alanine, strains PA374 and PA354 produced only about 0.2 g/l pantothenate in test tube cultures, indicating that PanD activity is significantly rate limiting.

- 20 To alleviate this limitation, the amplifiable P_{26} *panD* cassette from strain PA401 was installed. PA401 chromosomal DNA was transformed into PA374 and PA354, selecting for Tet^r at 15 mg/l, to yield strains PA377 and PA365, respectively. After transformants were obtained, the strains were streaked on plates containing 30 and 60 mg/l tetracycline to reamplify the copy number of the P_{26} *panD* cassette integrated at the *bpr* locus. In test tube cultures grown in SVY without α -KIV or β -alanine, a substantial improvement in pantothenate titers over those of PA374 and PA354 was obtained (Tables 18 and 19).

Table 18. *Pantothenate production by PA365, containing amplified P₂₆ panD, and controls, in 24 and 36 hr test tube cultures grown in SVY-glucose without β -alanine or α -KIV.*

Strain	Relevant genotype	OD ₆₀₀		[pan] g/l	
		24 hrs.	36 hrs	24 hrs.	36 hrs.
PA342-1-1	w.t. <i>ilvD</i>	11.7	8.8	b.d.	0.27
PA342-1-2	w.t. <i>ilvD</i>	12.8	8.8	b.d.	0.26
PA354-1-1	P ₂₆ <i>ilvD</i>	n.d.	11.0	n.d.	0.19
PA354-1-2	P ₂₆ <i>ilvD</i>	n.d.	8.4	n.d.	0.20
PA365-1	P ₂₆ <i>ilvD</i> , P ₂₆ <i>panD</i>	9.8	10.0	1.01	2.07
PA365-2	P ₂₆ <i>ilvD</i> , P ₂₆ <i>panD</i>	9.9	10.4	0.96	2.09

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n.d. = not determined; b.d. = below detection

Table 19. *Pantothenate production by PA377, containing amplified P₂₆ panD, and controls, in 27 hr test tube cultures grown in SVY-glucose or SVY-maltose, without α -KIV, and with or without β -alanine.*

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Strain	Relevant genotype	OD ₆₀₀			
		- β -ala Glucose	+ β -ala Glucose	- β -ala Maltose	+ β -ala Maltose
PA374-1	P ₂₆ <i>ilvD</i>	9.4	9.8	7.0	6.4
PA374-2	P ₂₆ <i>ilvD</i>	9.2	9.6	6.6	6.3
PA377-1	P ₂₆ <i>ilvD</i> , P ₂₆ <i>panD</i>	10.0	7.6	7.2	6.1
PA377-2	P ₂₆ <i>ilvD</i> , P ₂₆ <i>panD</i>	10.5	7.8	9.4	5.4

Strain	Relevant genotype	[pan] g/l			
		- β -ala Glucose	+ β -ala Glucose	- β -ala Maltose	+ β -ala Maltose
PA374-1	P ₂₆ <i>ilvD</i>	0.04	2.76	0.14	1.31
PA374-2	P ₂₆ <i>ilvD</i>	0.10	2.65	0.15	1.33
PA377-1	P ₂₆ <i>ilvD</i> , P ₂₆ <i>panD</i>	1.25	2.76	1.26	1.10
PA377-2	P ₂₆ <i>ilvD</i> , P ₂₆ <i>panD</i>	1.25	2.35	1.31	1.26

15 In SVY with glucose, an increase in pantothenate production can still be achieved by feeding 5 g/l β -alanine suggesting that increasing *panD* expression further might increase pantothenate production. In SVY with maltose, no further increase in pantothenate was obtained by feeding β -alanine suggesting that β -alanine and/or

aspartate synthesis is suppressed by glucose. Strains PA377 and PA365 have been evaluated in 10 liter fermentors, where they typically produce above 20 g/l pantothenate in 48 hours without supplemental β -alanine and α -KIV or valine, described in detail below.

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EXAMPLE X: 10 liter Fermentations of Pantothenate-Producing Microbes

Engineering of the P_{26} *ilvBNC* and P_{26} *ilvD* cassettes to give strains PA342 and PA354 allowed the production of 22 and 26 g/l of pantothenate, respectively, without the addition of valine or α -KIV to the fermentation medium (Table 20). At 48 hours, both strains had secreted about 0.5 g/l of valine into the medium.

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Table 20. 10-liter fermentations of five pantothenate overproducing strains.

Strain	Medium	Feed 40% Glucose plus	OD 600 48 hr	Valine 48 hours g/l	β -ala 48 hr g/l	Pantothenate g/L		
						36 hr	48 hr	72 hr
PA 236	SVYG	50 g/l β -ala 25 g/l α -KIV	108	added	added	16	19	21
PA 342	SVYG	50 g/l β -ala	92	0.5	added	17	22	--
PA 354	SVYG	50 g/l β -ala	90	0.5	added	19	26	--
PA 365	SVYG	25g/l YE	77	0.85	0.4	18	21	27
PA 377	SVYG	25g/l YE	85	1.5	0.5	18	22	31
PA 377	PFMG	25g/l YE	96	0.8	0.4	19	25	29
PA377	PFMG	-	71	0.7	0.1	16	21	-

15 Pantothenate synthesis in fermentors

With the addition of the P_{26} *panD* cassette to strains PA354 and PA374 to create strains PA365 and PA377, neither β -alanine nor α -KIV needed to be added to the fermentors. Strain PA365 produced 21 g/l pantothenate in 48 hours and 27 g/l in 72 hours with no precursors added to the medium (Table 20). PA377 was somewhat better, producing 18 g/l of pantothenate in 36 hours, 22 g/l in 48 hours, and 31 g/l in 72 hours). Valine was measured at 0.85 and 1.5 g/l for strains PA365 and PA377, respectively, at

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48 hours in SVYG medium. Strain PA377 maintained valine between 1-1.5 g/l throughout most of the fermentation and β -alanine between 0.2 and 0.5 g/l.

Strain PA377 was further evaluated in 10-liter fermentors in yeast extract based PFMG medium. Pantothenate yields in PFMG and SVYG medium were similar. In PFMG, PA377 produced 19 g/l of pantothenate in 36 hours, 25 g/l in 48 hours, and 29 g/l in 72 hours. In SVYG, PA377 produced 18 g/L pantothenate in 36 hours, 22 g/L in 48 hours and 31 g/L in 72 hours (Table 20).

EXAMPLE XI: Converting Strain PA377 to a Tryptophan Prototroph

PA377 (Trp^-) was transformed to Trp^+ using chromosomal DNA from PY79 to give strain PA824. After re-amplification of the $P_{26}panD$ cassette, PA824 was compared to PA377 for pantothenate production in test tube cultures grown in SVY glucose with or without 5 g/L β -alanine (Table 21).

Table 21 : *Trp⁺ derivatives of PA377: Pantothenate production in 48 hour test tube cultures grown in SVY glucose, $\pm\beta$ -alanine*

Strain	<i>trpC</i> donor	OD ₆₀₀		[pan] g/L	
		- β -alanine	+ β -alanine	- β -alanine	+ β -alanine
PA377-1	RL-1	8	8	1.5	3.4
PA377-2	RL-1	8	9	1.6	3.6
PA824-1	PY79	12	10	0.7	3.7
PA824-2	PY79	11	11	1.9	4.9

The Trp^+ strains grew to slightly higher densities than PA377. In the absence of exogenous β -alanine, all of the strains produced similar levels of pantothenate, while with the addition of β -alanine, the Trp^+ derivatives produced somewhat more pantothenate.

25 Fermentor studies with PA824

PA824 was evaluated in CF3000 Chemap 14 liter vessels with 10 liter working volumes. Formulations for two of the media used in the fermentors are given in Tables 22 and 23.

Table 22 : Formulation for PFMG-5 medium

BATCH		
	MATERIAL	g/L (final [I])
1	Amberex 1003	10
2	Na Glutamate	5
3	(NH ₄) ₂ SO ₄	8
4	MAZU DF 37C	2.5
Added After Sterilization and Cool Down		
1	KH ₂ PO ₄	10
2	K ₂ HPO ₄ ·3H ₂ O	20
1	Glucose	20
2	MgCl ₂ ·6H ₂ O	1
3	CaCl ₂ ·2H ₂ O	0.1
1	Sodium Citrate	1
2	FeSO ₄ ·7H ₂ O	0.01
3	SM-1000X	1.0 ml
	H ₂ O	qs to 6000 ml

5

FEED		
	MATERIAL	g/L
1	Glucose	600
2	CaCl ₂ ·2H ₂ O	0.6
	H ₂ O	qs to 3000 ml

Table 23 : Formulation for SVY-4 medium

BATCH		
	MATERIAL	g/L (final [I])
1	Veal Infusion	25
2	Yeast Extract	5
3	Na Glutamate	5
4	(NH ₄) ₂ SO ₄	4
5	MAZU DF 37C	2.5

Added After Sterilization and Cool Down

1	KH ₂ PO ₄	10
2	K ₂ HPO ₄ ·3H ₂ O	20
1	Glucose	20
2	MgCl ₂ ·6H ₂ O	1
3	CaCl ₂ ·2H ₂ O	0.1
1	Sodium Citrate	1
2	FeSO ₄ ·7H ₂ O	0.01
3	SM-1000X	1.0 ml
	H ₂ O	qs to 6000 ml

5

FEED

	MATERIAL	g/L
1	Glucose	600
2	CaCl ₂ ·2H ₂ O	0.6
	H ₂ O	qs to 3000 ml

All fermentations were glucose limited fed batch processes. Immediately after inoculation, agitation was set at 200 rpm. The initial batched 2% glucose was consumed during exponential growth. Afterwards, glucose concentrations were maintained

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between 0.2 and 1.0 g/L by continuous feeding of a 60% glucose solution. The variable rate feed pump was computer controlled and linked to the dissolved oxygen concentration [pO₂] in the tank by an algorithm. When the [pO₂] fell to 30%, computer control began to automatically adjust the agitation rate to maintain a dissolved oxygen concentration between 25 and 30% [pO₂]. Computer control and data recording were by Braun MFCS software.

In one study, PA284 was grown in fermentors at two temperatures (40°C and 43°C) in the medium described in Table 22. Results of two experiments demonstrated that the highest pantothenate titers at early time points were produced at 43°C. The cell mass approached 150 optical density units at OD₆₀₀ and 56 hours at 43°C, and the pantothenate titers were 21 g/L, 28 g/L and 36 g/L at 36, 48 and 72 hours respectively. In the parallel fermentation at 40°C, the cell mass approached 120 optical density units at OD₆₀₀ and 56 hours, and the pantothenate titers were 18 g/L, 26 g/L and 37 g/L at 36, 48 and 72 hours, respectively.

In another study, PA824 was grown in a fermentor at 43°C in the medium described in Table 23. The cell mass exceeded 160 optical density units at OD₆₀₀ and 36 hours, and the pantothenate titers were 23 g/L, 34 g/L, 37 g/L and 40 g/L at 24, 36, 48 and 60 hours, respectively. In other fermentations, increasing the amount of trace elements in the glucose feed (e.g., increasing the concentration of SM from 1X to 2X) resulted in even higher titers of pantothenate.

EXAMPLE XII: Identification and characterization of the *B. subtilis* *coaA* gene product

The annotated version of the *B. subtilis* genome sequence available on the "Subtilist" web site contains no gene labeled as *coaA*. However a homology search using the protein sequence of *E. coli* pantothenate kinase as a query sequence gave a good match with *B. subtilis* gene *yqjS*, which is annotated as "unknown; similar to pantothenate kinase." This gene appears to be the penultimate gene in an operon containing five open reading frames (Figure 18). Two of the open reading frames encode proteins which are similar to D-serine dehydratase and to "ketoacyl reductase"; the other two have no known homologies. For the open reading frame corresponding to *coaA*, there are three possible start codons; each having a possible ribosome-binding site (RBS) associated with it. The three potential *coaA* ORFs were named *coaA1*, *coaA2*, and *coaA3*, from longest to shortest.

All three potential *coaA* open reading frames were cloned along with their respective RBSs by PCR followed by ligation into expression plasmid pAN229. pAN229 is a low copy vector in *E. coli* that provides expression from the SP01 phage *P₁₅* promoter and can integrate by single crossover at *bpr* with tetracycline selection. A
5 representative resulting plasmid, pAN281, is shown in Figure 19.

To determine if the cloned putative *coaA* ORFs actually encode a pantothenate kinase activity, several isolates of all three plasmids were transformed into the *E. coli* strain YH1, that contains the *coaA15(Ts)* allele. Transformants were streaked to plates incubated at 30° and 43°C to test for complementation of the temperature sensitive
10 allele. All isolates of all three *coaA* variants, except for one isolate of pAN282, complemented well at 43°C, indicating that all three plasmid constructs encode an active pantothenate kinase. Accordingly, it can be concluded that the *B. subtilis yqjS* open reading frame codes for an active pantothenate kinase.

15 **EXAMPLE XIII: Deletion of the *coaA* gene from the *B. subtilis* genome**

The *coaA* gene of *B. subtilis* (*yqjS*) was deleted from the chromosome of a *B. subtilis* strain by conventional means. The majority of the *coaA* coding sequence was deleted from a plasmid clone and replaced by a chloramphenicol resistance gene (*cat*), while leaving approximately 1 kb of upstream and downstream sequence to allow
20 homologous recombination within the chromosome, to give plasmid pAN296 (see Figure 17). pAN296 was then used to transform a *B. subtilis* strain (PY79), selecting for chloramphenicol resistance. The majority of transformants result from a double crossover event that effectively substitutes the *cat* gene for the *coaA* gene. The transformed strain containing the *coaA* deletion – *cat* insertion grew normally due the
25 presence of a second *B. subtilis* pantothenate kinase encoding gene described herein.

EXAMPLE XIV: Identification and characterization of a second *B. subtilis* gene encoding pantothenate kinase activity

As described in detail in the instant specification, in order to maximize
30 pantothenate production, it is necessary to restrict the flow of pantothenate toward Coenzyme A (CoA), for example, by reducing the activity of pantothenate kinase, the first enzyme in the pathway from pantothenate to CoA. After finding that deletion of the *coaA* gene from the chromosome of *B. subtilis* is not a lethal event (see Example XIII), it was concluded that *B. subtilis* must contain a second gene that encodes an active
35 pantothenate kinase, since pantothenate kinase is an essential enzyme activity.

A second pantothenate kinase-encoding gene was identified by complementing the *E. coli* strain YH1 (*coaA15(Ts)*) with a *B. subtilis* gene bank and selecting for transformants that were able to grow at 43°C. Found among the transformants were two families of plasmids that had overlapping restriction maps within each family, but not
5 between the families. As expected, the restriction map of one family was identical to that predicted from the *B. subtilis* genome sequence for the homologue of the *E. coli* *coaA* gene (which we named *coaA* also, see above) and surrounding sequences. The other family had a restriction map that was completely non-overlapping with the first.

DNA sequencing of the ends of the cloned inserts from the second family
10 showed that the clones came from a region of the *B. subtilis* chromosome that includes the 3' end of the *ftsH* gene, the 5' end of the *sul* gene, and all of the *yacB*, *yacC*, *yacD*, *cysK*, *pabB*, *pabA* and *pabC* genes. None of the open reading frames of these cloned inserts showed homology to any known pantothenate kinase sequences, either prokaryotic or eukaryotic.

15 Several deletions were created through the *B. subtilis* genomic sequences in the cloned inserts. Each deletion was tested for complementation of the *E. coli* temperature sensitive pantothenate kinase. In particular, a deletion that removed all DNA between a *Stu* I site in the cloning vector and a *Swa* I site in the *yacC* gene, leaves *yacB* as the only intact open reading frame in the cloned insert (see Figure 21). This deleted plasmid still
20 complemented the *E. coli* pantothenate kinase mutant. However, another deletion that removed DNA from the *Swa* I site in *yacC* through a *Bst* I 107I site in the (already truncated) *ftsH* gene, could not complement the *E. coli* pantothenate kinase mutant. From these results, it was concluded that the *yacB* open reading frame was responsible for the complementation activity. To confirm that *yacB* is a pantothenate kinase gene,
25 the *yacB* ORF plus 112 base pairs of downstream flanking sequence was amplified by PCR in two independent reactions and cloned downstream of a constitutive promote to give plasmids pAN341 and pAN342 (Figure 22). Both pAN341 and pAN342 complemented the defect in YH1 at 44°C, while a control plasmid, which has the same backbone, but expresses *panBCD* instead of *yacB* did not. This confirmed that the *yacB*
30 open reading frame was responsible for the complementation of YH1.

As such, a novel gene that encodes pantothenate kinase activity in *B. subtilis* has been discovered that is not related by homology to any previously known pantothenate kinase gene. This gene has been renamed *coaX*, as a second, alternative gene that encodes an enzyme that catalyzes the first step in the pathway from pantothenate to
35 CoaA. Deletion of *coaX* by methods described above for deleting *coaA*, in conjunction

with reduction in the activity of the CoaA enzyme, provides a means to reduce pantothenate kinase activity to the desired level.

Several homologues of the *B. subtilis* *coaX* gene were identified by homology searching of various publically available databases using the published *yacB* (*coaX*) open reading frame sequence and predicted amino acid sequence (as set forth in SEQ ID NOs:84 and 85 respectively). In two cases (*Mycobacterium tuberculosis* and *Streptomyces coelicolor*) the homologous *coaX* genes are adjacent to, or almost adjacent to, pantothenate biosynthetic genes, consistent with these homologs having a role in pantothenate metabolism. The CoaX proteins show no homology to the CoaA family of pantothenate kinases, nor to the eukaryotic family of pantothenate kinases exemplified by PanK of *Saccharomyces cerevisiae*.

Alignment of the amino acid sequences of several bacterial CoaX homologs with the amino acid sequence predicted from translating the *B. subtilis* *yacB* ORF described in the published *B. subtilis* genome sequence revealed that the CoaX proteins from other bacteria contained additional amino acid residues at their carboxy-terminal ends. Moreover, these extensions beyond the end of the predicted amino acid for the *B. subtilis* gene product contained two relatively well conserved segments of sequence.

Translation of nucleotide sequences just downstream from the stop codon of the *B. subtilis* *yacB* ORF in a different reading frame revealed the existence of amino acid sequences very similar to the carboxy-terminal extensions of the other bacterial CoaX proteins. It is thus believed that an error exists in the published DNA sequence of the *B. subtilis* *yacB* ORF sequence that causes a frame shift leading to an artifactual downstream amino acid sequence and premature termination.

The PCR-generated sequences of *B. subtilis* *CoaX* in pAN341 and pAN342 (described above) contain enough downstream flanking sequence to encode the putative carboxy-terminal extension described above, which is consistent with the result that the clones were functional in the complementation assay. However when the 3' PCR primer was positioned to include only the shorter *yacB* ORF predicted from the published sequence, but not to include the putative carboxy-terminal extension, then the resulting plasmids, pAN329 and pAN330 (similar in structure to pAN341 and pAN342; see Figure 22), did not complement the defect in YH1. This result supports the notion that the published *yacB* coding sequence contains a frame-shift error, and that the carboxy-terminal end of CoaX is necessary for pantothenate kinase activity. The predicted correct nucleotide sequence for *B. subtilis* *coaX* is set forth as SEQ ID NO:19 and the translated amino acid sequence is set forth as SEQ ID NO:9. A multiple

EXAMPLE XVIII: Generation of mutant *coaX* genes encoding pantothenate kinase having reduced or temperature sensitive activities

Mutant *coaX* genes are generated by introducing point mutations into the gene and testing the resulting mutants for the ability to complement the *E. coli* YH1 strain as described in Example XII. Preferred mutations in the *coaX* gene sequences are those that encode a substitution of a residue conserved among CoaX sequences from a variety of bacterial sources (e.g., a conserved residue set forth in Figure 23). Alternatively, random mutations in the *coaX* gene sequence are generated by mutagenic PCR and *in vitro* recombination and identified by screening for alleles that poorly complement the *E. coli coaA15(Ts)* mutant.

Mutants so generated (i.e., mutants having reduced *coaX* activity) can be further engineered such that the endogenous *coaA* gene is deleted (as described in Example XIII). CoaX reduced-activity mutants can also be further engineered to contain reduced-activity CoaA gene products as described in Example XV.

EXAMPLE XIX: Enhanced Production of Panto-Compounds Using Bacteria Having Deletions in One or More Pantothenate Biosynthetic Enzymes

If the desired panto-compound is not pantothenate, then an appropriate deletion of one or more of the pantothenate biosynthetic genes from a pantothenate overproducing strain will provide a strain that produces said desired panto-compound. In this example, the desired panto-compound is pantoate. Starting with, for example, strain PA236, PA313 or PA824 either one or both of the *panC* and *panD* genes is deleted. In another example, ketopantoate is the desired panto-compound. Starting with, for example strain PA244, PA245 or PA824 one, two or all of the *ilvC*, *panE1*, *panC* and *panD* genes are deleted from the starting strain. If β -alanine is the desired panto-compound, then *panB* and *panC* can be deleted, preferably in a fashion that leaves an in frame fusion of a small portion of the 5' end of *panB* with a small portion of the 3' end of *panC*, from the strain PA221, PA235, PA245, or PA313. In all of the above-mentioned examples, the panto-compound producing strain will be a pantothenate auxotroph. Accordingly, the growth medium requires sufficient pantothenate for adequate growth. Vectors designed to overexpress *panD* as described above are then transformed into the above strains to further enhance β -alanine production.

The above-mentioned deletions are accomplished by methods well-known to those skilled in the art, for example, by insertion of an antibiotic resistance gene and removing sufficient sequence from the target gene(s) to inactivate said target gene(s).

Alternatively, removal of targeted sequences is accomplished without simultaneous introduction of an antibiotic resistance gene in said target gene and then introduced by congression (co-transformation with any other appropriate selectable DNA sequence) followed by screening for the loss of function of said target gene by replica plating.

5

Table 24 : Strains (and corresponding phenotypes) for panto-compound production

Name	Pheno type	Drug resist.	<i>panBCD</i> locus	<i>panE</i> locus	<i>ilvD</i> locus	<i>amyE</i> locus	<i>bpr</i> locus	Parent
PA221	Trp-		<i>P26panBCD</i>					
PA222			<i>P₁₅ panBCD</i>					RL-1
PA235			<i>P26panBCD</i>					
PA236			<i>P₂₆ panBCD</i>	<i>P₂₆ panE1</i>				PA221
PA327	Trp-		<i>P26panBCD</i>	<i>P26panE1</i>				PA221
PA328	Trp-		<i>P26panBCD</i>	<i>P26panE1</i>				PA235
PA340	Trp-	Spc	<i>P26panBCD</i>	<i>P26panE1</i>		<i>P26ilvBNC</i>		PA327
PA342	Trp-	Spc	<i>P26panBCD</i>	<i>P26panE1</i>		<i>P26ilvBNC</i>		PA328
PA354	Trp-	Spc	<i>P26panBCD</i>	<i>P26panE1</i>	<i>P26ilvD</i>	<i>P26ilvBNC</i>		PA342
PA365	Trp-	Spc, Tet	<i>P26panBCD</i>	<i>P26panE1</i>	<i>P26ilvD</i>	<i>P26ilvBNC</i>	<i>P26panD423</i>	PA354
PA374	Trp-	Spc	<i>P26panBCD</i>	<i>P26panE1</i>	<i>P26ilvD</i>	<i>P26ilvBNC</i>		PA340
PA377	Trp-	Spc, Tet	<i>P26panBCD</i>	<i>P26panE1</i>	<i>P26ilvD</i>	<i>P26ilvBNC</i>	<i>P26panD423</i>	PA374
PA401	Trp-		<i>P26panBCD</i>				<i>P26panD423</i>	PA221
PA402	Trp-		<i>P26panBCD</i>				<i>P26panD428</i>	PA221
PA403	Trp-		<i>P26panBCD</i>				<i>P26panD429</i>	PA221
PA404	Trp-	Spc, Tet	<i>P26panBCD</i>	<i>P26panE1</i>		<i>P26ilvBNC</i>	<i>P26panD423</i>	PA340
PA405	Trp-	Spc, Tet	<i>P26panBCD</i>	<i>P26panE1</i>		<i>P26ilvBNC</i>	<i>P26panD423</i>	PA342
PA651	Trp-	Spc	<i>P26panBC*D</i>	<i>P26panE1</i>	<i>P26ilvD</i>	<i>P26ilvBNC</i>		PA374
PA284		Spc, Tet	<i>P26'panBCD</i>	<i>P26panE1</i>	<i>P26ilvD</i>	<i>P26ilvBNC</i>	<i>P26panD423</i>	PA377

Equivalents Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

10

What is claimed:

1. A method of producing a panto-compound comprising culturing a microorganism which overexpresses at least one *Bacillus* pantothenate biosynthetic enzyme under conditions such that the panto-compound is produced.
2. The method of claim 1, wherein the microorganism overexpresses at least one *Bacillus subtilis* pantothenate biosynthetic enzyme.
3. The method of claim 1 or 2, wherein the pantothenate biosynthetic enzyme is selected from the group consisting of ketopantoate hydroxymethyltransferase, pantothenate synthetase, aspartate- α -decarboxylase and ketopantoate reductase.
4. The method of any one of claims 1 to 3, wherein the microorganism overexpresses at least two pantothenate biosynthetic enzymes.
5. The method of any one of claims 1 to 3, wherein the microorganism overexpresses at least three pantothenate biosynthetic enzymes.
6. The method of any one of claims 1 to 5, wherein the panto-compound is selected from the group consisting of pantothenate, pantoate, ketopantoate and β -alanine.
7. A method of producing a panto-compound comprising culturing a ketopantoate reductase-overexpressing (KPAR-O) microorganism under conditions such that the panto-compound is produced.
8. The method of claim 7, wherein the panto-compound is pantothenate or pantoate.
9. The method of claim 7 or 8, wherein the ketopantoate reductase is bacterial-derived.
10. The method of claim 7 or 8, wherein the ketopantoate reductase is derived from *Bacillus*.

11. The method of claim 7 or 8, wherein the ketopantoate reductase is derived from *Bacillus subtilis*.

12. The method of any one of claims 7 to 11, wherein the KPAR-O
5 microorganism further overexpresses at least one pantothenate biosynthetic enzyme in addition to overexpressing ketopantoate reductase.

13. The method of claim 12, wherein the KPAR-O microorganism further
10 overexpresses at least one of ketopantoate hydroxymethyltransferase, pantothenate synthetase and aspartate- α -decarboxylase.

14. A method of producing pantothenate in a manner independent of
precursor feed comprising culturing an aspartate- α -decarboxylase-overexpressing (A α D-O) microorganism having a deregulated isoleucine-valine (*ilv*) pathway under conditions
15 such that pantothenate is produced.

15. A method of producing at least 2 g/L pantothenate in a manner
independent of aspartate or β -alanine feed comprising culturing an aspartate- α -
decarboxylase-overexpressing (A α D-O) microorganism under conditions such that
20 pantothenate is produced.

16. A method of producing at least 2 g/L pantothenate in a manner
independent of valine or α -ketoisovalerate feed comprising culturing a microorganism
having a deregulated isoleucine-valine (*ilv*) biosynthetic pathway under conditions such
25 that pantothenate is produced.

17. A method of producing at least 30 g/L pantothenate in a manner
independent of aspartate or β -alanine feed comprising culturing an aspartate- α -
decarboxylase-overexpressing (A α D-O) microorganism under conditions such that
30 pantothenate is produced.

18. A method of producing at least 30 g/L pantothenate in a manner
independent of valine or α -ketoisovalerate feed comprising culturing a microorganism
having a deregulated isoleucine-valine (*ilv*) biosynthetic pathway under conditions such
35 that pantothenate is produced.

19. A β -alanine independent high yield production method for producing pantothenate comprising culturing a manipulated microorganism under conditions such that pantothenate is produced at a significantly high yield.

5 20. The method of any one of claims 14 to 19, wherein the microorganism overexpresses acetohydroxyacid synthetase or is transformed with a vector comprising an *ilvBN* nucleic acid sequence or an *alsS* sequence.

10 21. The method of any one of claims 14 to 19, wherein the microorganism overexpresses acetohydroxyacid isomeroreductase or is transformed with a vector comprising an *ilvC* nucleic acid sequence.

15 22. The method of any one of claims 14 to 19, wherein the microorganism overexpresses dihydroxyacid dehydratase or is transformed with a vector comprising an *ilvD* nucleic acid sequence.

20 23. The method of any one of claims 19 to 22, wherein the microorganism overexpresses aspartate- α -decarboxylase or is transformed with a vector comprising a *panD* nucleic acid sequence.

24. The method of any one of claims 14 to 23, wherein the microorganism further has a deregulated pantothenate biosynthetic pathway.

25 25. The method of any one of claims 14 to 24, wherein the microorganism further has at least one mutant gene selected from the group consisting of a mutant *avtA* gene, a mutant *ilvE* gene, a mutant *ansB* gene and a mutant *alsD* gene.

30 26. The method of claim 24, wherein the microorganism overexpresses any of ketopantoate hydroxymethyltransferase, ketopantoate reductase, pantothenate synthetase and aspartate- α -decarboxylase.

35 27. The method of claim 24 or 26, wherein the microorganism is transformed with a vector comprising a *panBCD* nucleic acid sequence or a vector comprising a *panEI* nucleic acid sequence.

28. The method of any one of claims 14 to 16 and 19 to 27, wherein pantothenate is produced at a level selected from the group consisting of a level greater than 10g/L, a level greater than 20g/L and a level greater than 40g/L.

5 29. The method of claim 20, wherein the microorganism overexpresses acetohydroxyacid synthetase derived from *Bacillus* or is transformed with a vector comprising an *ilvBN* nucleic acid sequence or an *alsS* nucleic acid sequence derived from *Bacillus*.

10 30. The method of claim 21, wherein the microorganism overexpresses acetohydroxyacid isomeroreductase derived from *Bacillus* or is transformed with a vector comprising an *ilvC* nucleic acid sequence derived from *Bacillus*.

15 31. The method of claim 22, wherein the microorganism overexpresses dihydroxyacid dehydratase derived from *Bacillus* or is transformed with a vector comprising an *ilvD* nucleic acid sequence derived from *Bacillus*.

20 32. The method of claim 23, wherein the microorganism overexpresses aspartate- α -decarboxylase derived from *Bacillus* or is transformed with a vector comprising a *panD* nucleic acid sequence derived from *Bacillus*.

25 33. The method of claim 24 or 26, wherein the microorganism overexpresses any of ketopantoate hydroxymethyltransferase, ketopantoate reductase, pantothenate synthetase and aspartate- α -decarboxylase derived from *Bacillus*.

34. The method of claim 27, wherein the vector comprises a *panBCD* nucleic acid sequence or a *panEI* nucleic acid sequence derived from *Bacillus*.

30 35. A method of producing a panto-compound comprising contacting a composition comprising at least one pantothenate biosynthesis pathway precursor or isoleucine-valine biosynthesis pathway precursor with at least one isolated *Bacillus* enzyme selected from the group consisting of ketopantoate hydroxymethyltransferase, ketopantoate reductase, pantothenate synthetase and aspartate- α -decarboxylase, under conditions such that the panto-compound is produced.

35

36. A method of producing β -alanine comprising culturing an aspartate- α -decarboxylase-overexpressing (A α D-O) microorganism under conditions such that β -alanine is produced.

5 37. The method of claim 36, wherein the A α D-O microorganism has a mutation in a nucleic acid sequence encoding a pantothenate biosynthetic enzyme selected from the group consisting of ketopantoate hydroxymethyltransferase, ketopantoate reductase and pantothenate synthetase.

10 38. A method of producing β -alanine comprising contacting a composition comprising aspartate with an isolated *Bacillus* aspartate- α -decarboxylase enzyme under conditions such that β -alanine is produced.

15 39. A method for enhancing production of a panto-compound comprising culturing a mutant microorganism having a mutant *coaX* gene under conditions such that the panto-compound production is enhanced.

20 40. The method of claim 39, wherein said recombinant microorganism has a mutant *coaA* gene.

41. A method of producing a panto-compound comprising a pantothenate kinase mutant microorganism under conditions such that the panto-compound is produced at a significantly high yield.

25 42. The method of claim 41, wherein said mutant microorganism has a mutant *coaA* gene.

30 43. The method of claim 41, wherein said mutant microorganism has a mutant *coaX* gene.

44. The method of claim 41, where said mutant microorganism has a mutant *coaA* and *coaX* gene.

35 45. The method of any one of claims 39 to 44, wherein said panto-compound is selected from the group consisting of ketopantoate, pantoate or pantothenate.

46. The method of any one of claims 39 to 44, wherein said panto-compound is pantothenate.

47. The method of any one of claims 39 to 44, wherein said panto-compound is produced at a level selected from the group consisting of a level greater than 10g/L, a level greater than 20g/L and a level greater than 40g/L.

48. The method of any one of claims 39 to 44, wherein said recombinant microorganism further has a deregulated pantothenate biosynthetic pathway or further has a deregulated isoleucine-valine (*ilv*) biosynthetic pathway.

49. The method of claim any one of claims 39 to 44, wherein said recombinant microorganism further overexpresses *panD* and *panE*.

50. The method of any one of claims 39 to 44, wherein said recombinant microorganism further has at least one mutant gene selected from the group consisting of a mutant *avtA* gene, a mutant *ilvE* gene, a mutant *ansB* gene and a mutant *alsD* gene.

51. A method for enhancing production of a panto-compound comprising culturing a microorganism that has a deregulated pantothenate biosynthetic pathway and that also has a mutation that results in reduced pantothenate kinase activity under conditions such that the panto-compound production is enhanced.

52. A method for identifying compounds which modulate pantothenate kinase activity comprising contacting a recombinant cell expressing pantothenate kinase encoded by the *coaX* gene with a test compound and determining the ability of the test compound to modulate pantothenate kinase activity in said cell.

53. The method of claim 52, wherein said cell further comprises a mutant *coaA* gene encoding a pantothenate kinase having reduced activity.

54. The method of any one of claims 1 to 51, wherein the microorganism is Gram positive.

55. The method of any one of claims 1 to 51, wherein the microorganism is Gram negative.

56. The method of any one of claims 1 to 51, wherein the microorganism is a microorganism belonging to a genus selected from the group consisting of *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*.

5 57. The method of any one of claims 1 to 51 and 54 to 56, wherein the microorganism is of the genus *Bacillus*.

58. The method of any one of claims 1 to 51 and 54 to 57, wherein the microorganism is *Bacillus subtilis*.

10 59. The method of any one of claims 1 to 13, 35, 39 to 51 and 54 to 58, further comprising recovering the panto-compound.

15 60. The method of any one of claims 14 to 34 and 54 to 58, further comprising recovering the pantothenate.

61. The method of any one of claims 1 to 14, 35, 39 to 46, 48 to 51 and 54 to 59, wherein the panto-compound is produced at a level greater than 2 g/L.

20 62. A recombinant microorganism which overexpresses at least one *Bacillus* pantothenate biosynthetic enzyme.

63. The recombinant microorganism of claim 62, which overexpresses at least one *Bacillus subtilis* pantothenate biosynthetic enzyme.

25 64. The recombinant microorganism of claim 62 or 63, wherein the pantothenate biosynthetic enzyme is selected from the group consisting of ketopantoate hydroxymethyltransferase, pantothenate synthetase, aspartate- α -decarboxylase and ketopantoate reductase.

30 65. The recombinant microorganism of any one of claims 62 to 64, wherein the pantothenate biosynthetic enzyme is ketopantoate reductase.

66. A recombinant microorganism which overexpresses aspartate- α -decarboxylase and has a deregulated isoleucine-valine (*ilv*) biosynthetic pathway.

35

67. A recombinant microorganism having a mutant *coaX* gene, said mutant *coaX* gene encoding reduced pantothenate kinase activity in said microorganism.

5 68. The recombinant microorganism of claim 67 further having a mutant *coaA* gene, said mutant *coaA* gene encoding reduced pantothenate kinase activity in said microorganism.

69. A recombinant microorganism having a mutant *coaX* gene and optionally having a mutant *coaA* gene, said mutant microorganism having reduced pantothenate
10 kinase activity as compared to a microorganism having wild-type *coaA* and *coaX* genes.

70. A recombinant microorganism comprising a vector comprising an isolated *coaX* gene.

15 71. A recombinant microorganism that overproduces a panto-compound, the microorganism having a deregulated pantothenate biosynthetic pathway and having at least one mutation that results in a decrease in the capacity of the microorganism to synthesize Coenzyme A (CoA).

20 72. The recombinant microorganism of claim 71, having at least one mutation that results in a reduced level of pantothenate kinase activity.

73. The recombinant microorganism of claim 72, having a mutation in a *coaA* gene, or homologue thereof, that results in a reduced level of CoaA enzyme
25 activity.

74. The recombinant microorganism of claim 72, having a mutation in a *coaX* gene, or homologue thereof, that results in a reduced level of CoaX enzyme
30 activity.

75. The recombinant microorganism of claim 72, having a mutation in a *coaA* gene, or homologue thereof, and having a mutation in a *coaX* gene, or homologue thereof, the mutations resulting in reduced levels of CoaA enzyme activity and reduced
35 CoaX enzyme activity.

76. The recombinant microorganism of any one of claims 66 to 70 which further has a deregulated pantothenate biosynthetic pathway.

77. The recombinant microorganism of any one of claims 62 to 65 and 67 to 75, further having a deregulated isoleucine-valine (*ilv*) biosynthetic pathway.
- 5 78. The recombinant microorganism of any one of claims 62 to 77, which is Gram positive.
79. The recombinant microorganism of claim 78 belonging to a genus selected from the group consisting of *Bacillus*, *Cornyebacterium*, *Lactobacillus*,
10 *Lactococci* and *Streptomyces*.
80. The recombinant microorganism of claim 79 belonging to the genus *Bacillus*.
- 15 81. The recombinant microorganism of claim 80 which is *Bacillus subtilis*.
82. A recombinant microorganism selected from the group consisting of PA221, PA235, PA236, PA313, PA410, PA402, PA403, PA411, PA412, PA413, PA303, PA327, PA328, PA401, PA340, PA342, PA404, PA405, PA374, PA354,
20 PA365, PA377, PA651 and PA824.
83. A recombinant vector for use in the production of panto-compounds comprising a nucleic acid sequence which encodes at least one *Bacillus* pantothenate biosynthetic enzyme operably linked to regulatory sequences.
25
84. The vector of claim 83, comprising a nucleic acid sequence which encodes at least one *Bacillus subtilis* pantothenate biosynthetic enzyme.
85. The vector of claim 84, wherein the nucleic acid sequence encodes at
30 least one of ketopantoate hydroxymethyltransferase, pantothenate synthetase, aspartate- α -decarboxylase and ketopantoate reductase.
86. A recombinant vector comprising at least one nucleic acid sequence selected from the group consisting of SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27,
35 SEQ ID NO:29 and SEQ ID NO:59.

87. The vector of claim 84, wherein the nucleic acid sequence encodes ketopantoate reductase.

88. A vector comprising a mutant *coaX* gene, said mutant encoding a pantothenate kinase enzyme having reduced activity.

89. A vector comprising an isolated *coaX* gene.

90. A vector comprising an isolated *Bacillus coaX* gene.

91. A vector comprising an isolated *Bacillus subtilis coaX* gene.

92. The vector of any one of claims 86 and 89 to 91, which further comprises regulatory sequences.

93. The vector of any one of claims 83 to 85, 87 and 92, wherein the regulatory sequences comprise a constitutively active promoter.

94. The vector of claim 93, wherein the constitutively active promoter comprises P_{veg} (SEQ ID NO:41), P_{15} (SEQ ID NO:39) or P_{26} (SEQ ID NO:40) sequences.

95. The vector of claim 83, wherein the regulatory sequences comprise at least one artificial ribosome binding site (RBS).

96. The vector of claim 95, wherein the artificial RBS comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56 and SEQ ID NO:57.

97. A vector selected from the group consisting of pAN004, pAN005, pAN006, pAN236, pAN423, pAN428, pAN429, pAN441, pAN442, pAN443, pAN251, pAN267, pAN256, pAN257, pAN263, pAN240, pAN294, pAN296, pAN336, pAN341 and pAN342.

98. A recombinant microorganism comprising the vector of claim 86 or 93.

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99. An isolated nucleic acid molecule which encodes at least one *Bacillus* pantothenate biosynthetic gene.

100. The isolated nucleic acid molecule of claim 99 which encodes at least
5 one *Bacillus subtilis* pantothenate biosynthetic gene.

101. The isolated nucleic acid molecule of claim 99 or 100 which encodes ketopantoate reductase.

102. An isolated *Bacillus* pantothenate biosynthetic enzyme polypeptide.
10

103. An isolated *Bacillus subtilis* pantothenate biosynthetic enzyme
polypeptide.

104. An isolated *Bacillus* ketopantoate reductase polypeptide.
15

105. An isolated *Bacillus subtilis* ketopantoate reductase polypeptide.

106. An isolated *Bacillus* aspartate- α -decarboxylase polypeptide.
20

107. An isolated *Bacillus subtilis* aspartate- α -decarboxylase polypeptide.

108. An isolated nucleic acid molecule comprising a mutant *coaX* gene.

109. An isolated nucleic acid molecule comprising a *coaX* gene.
25

110. An isolated pantothenate kinase protein encoded by a *coaX* gene.

FIG.1

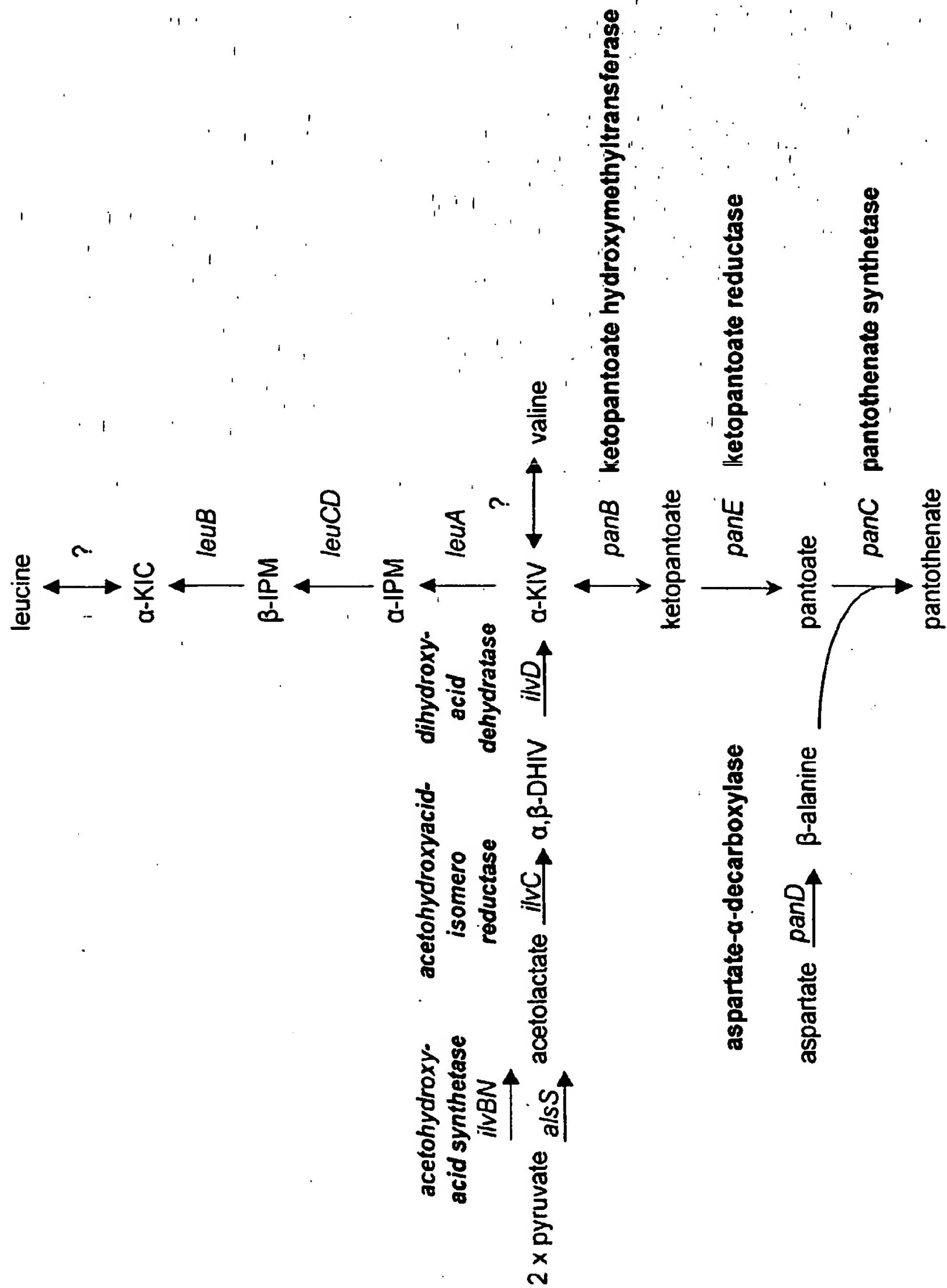


Figure 2. Plasmid pAN240, containing sequences ligated upstream of the P₂₆panBCD cassette, equivalent to the integrated version in strain PA221.

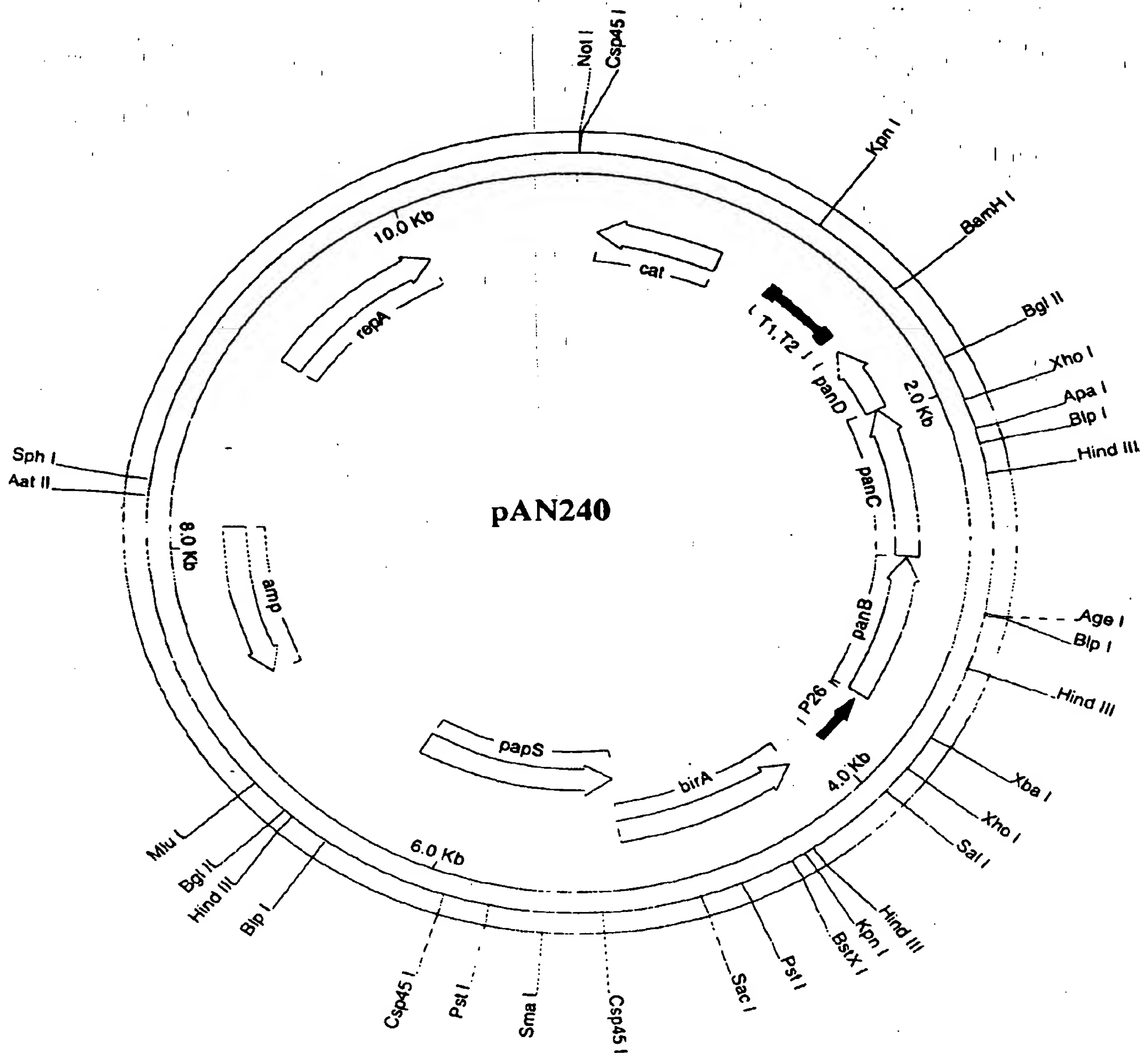


Figure 3A Plasmid pAN004, containing the panBCD operon expressed from P26 and RBS1.

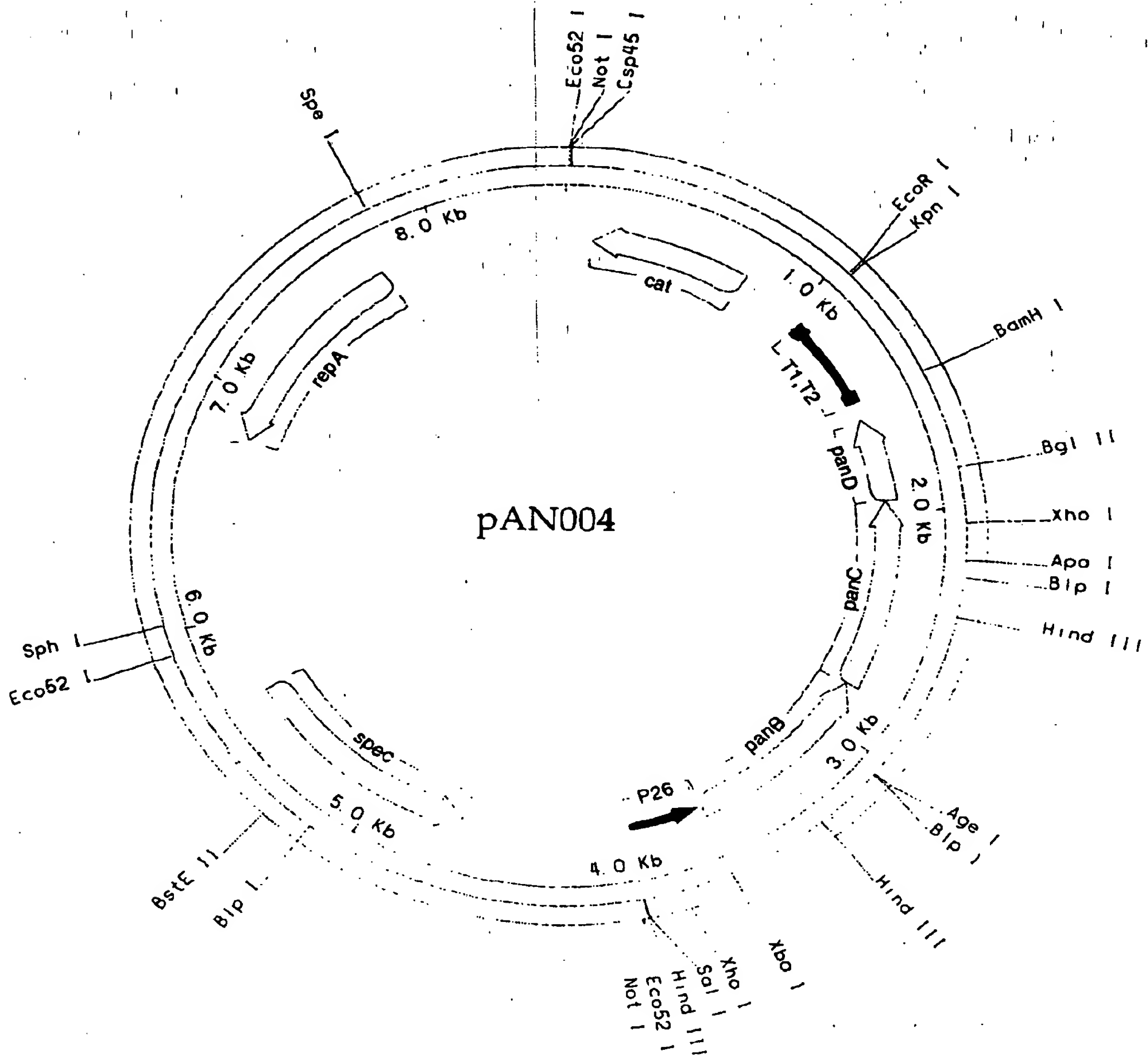


Figure 3 Plasmid pAN006, containing the panBCD operon expressed from P26 and RBS2.

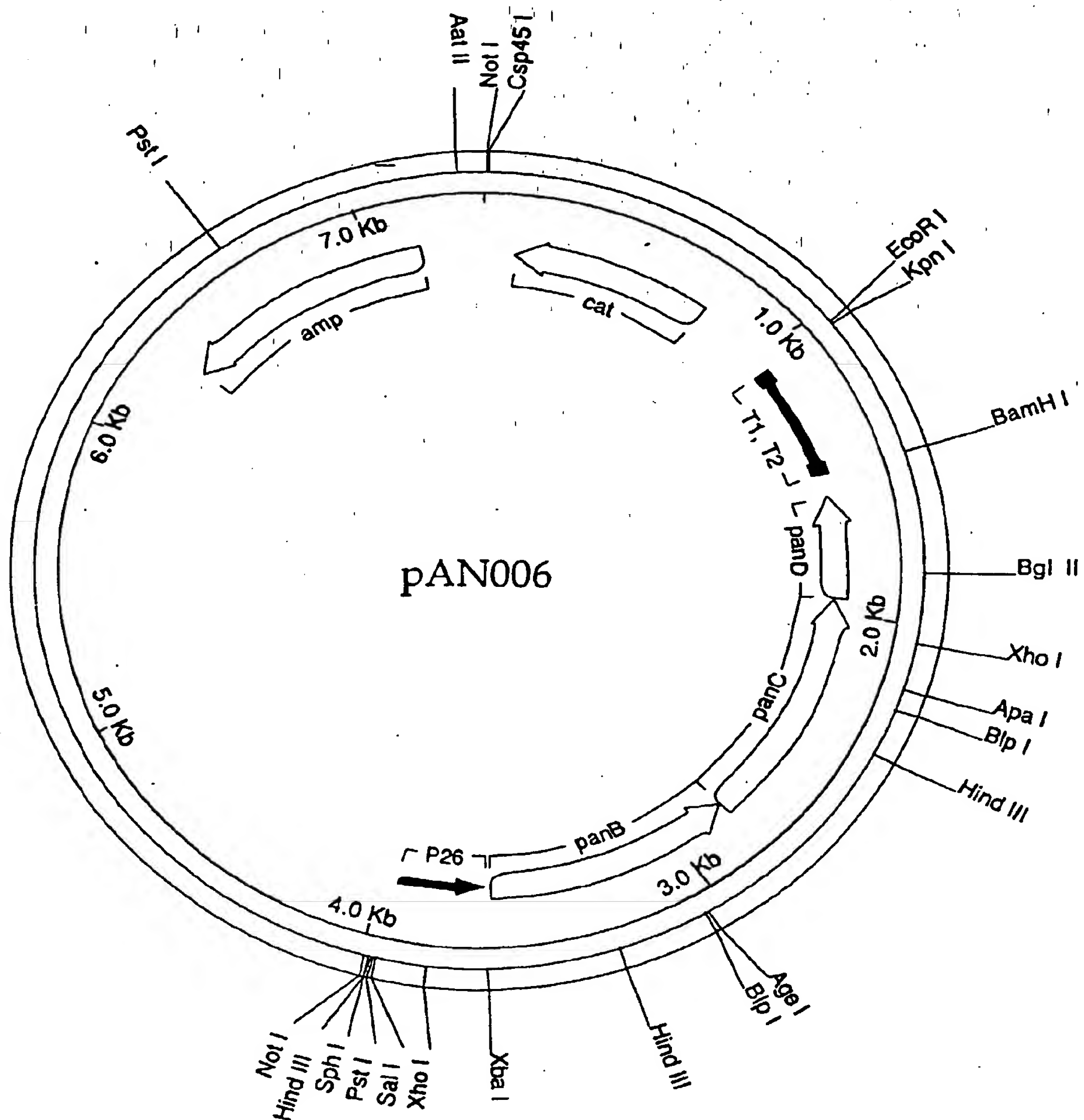


Figure 4 Plasmid pAN236, containing an integratable and amplifiable P26-RBS2-panE1 expression cassette.

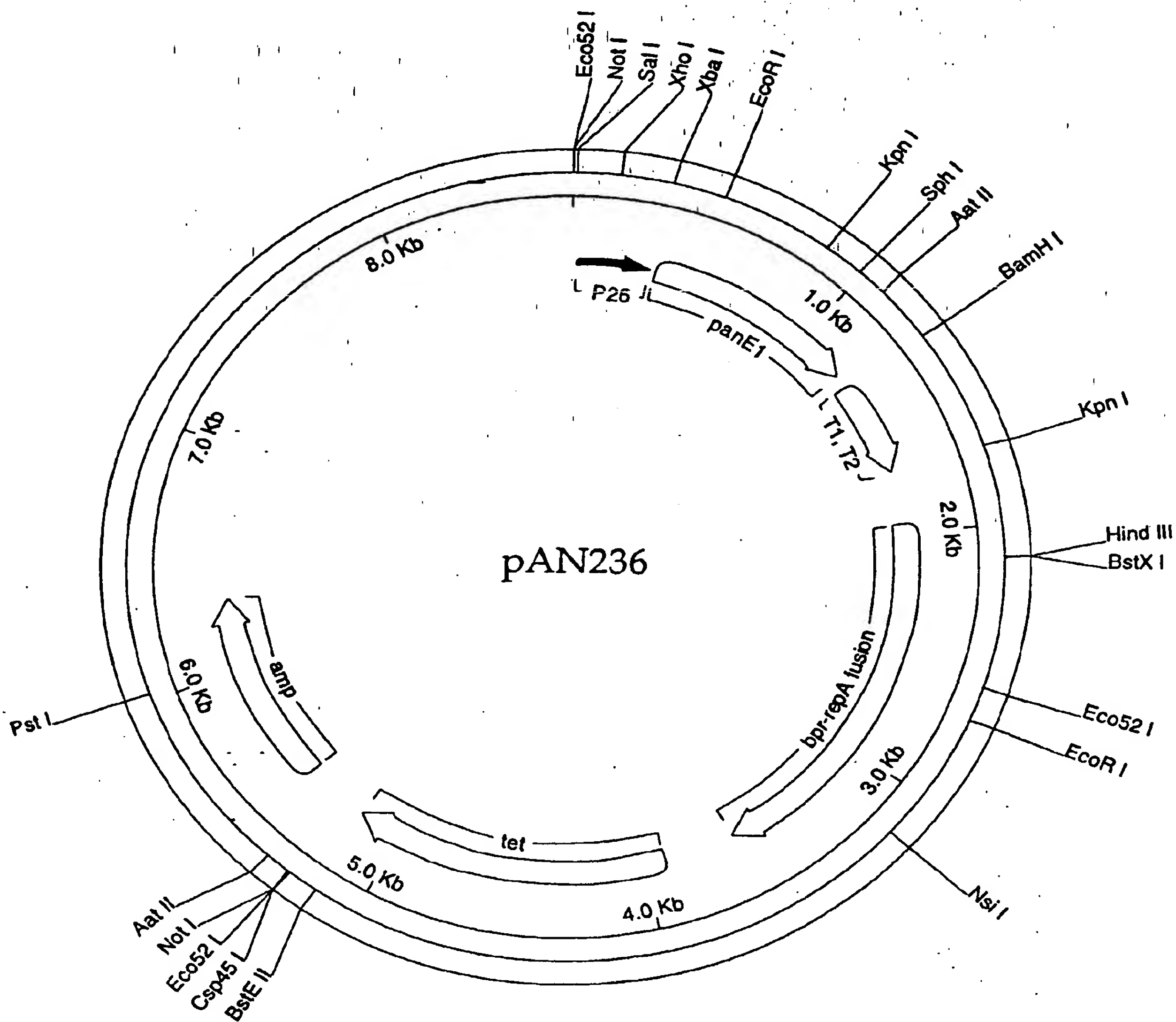


Figure 5 Construction of pAN423

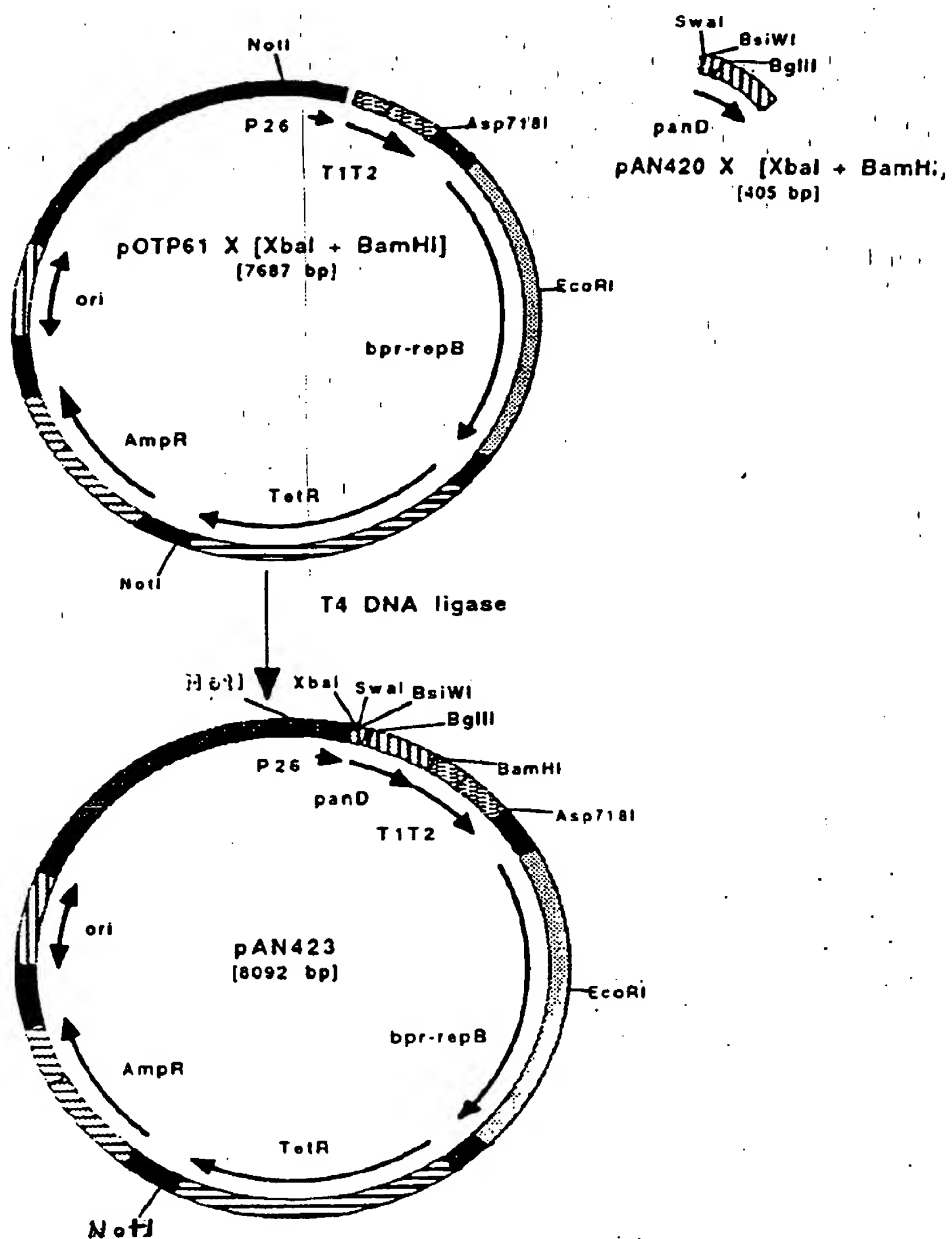


Figure 6 Construction of pAN426 and pAN427.

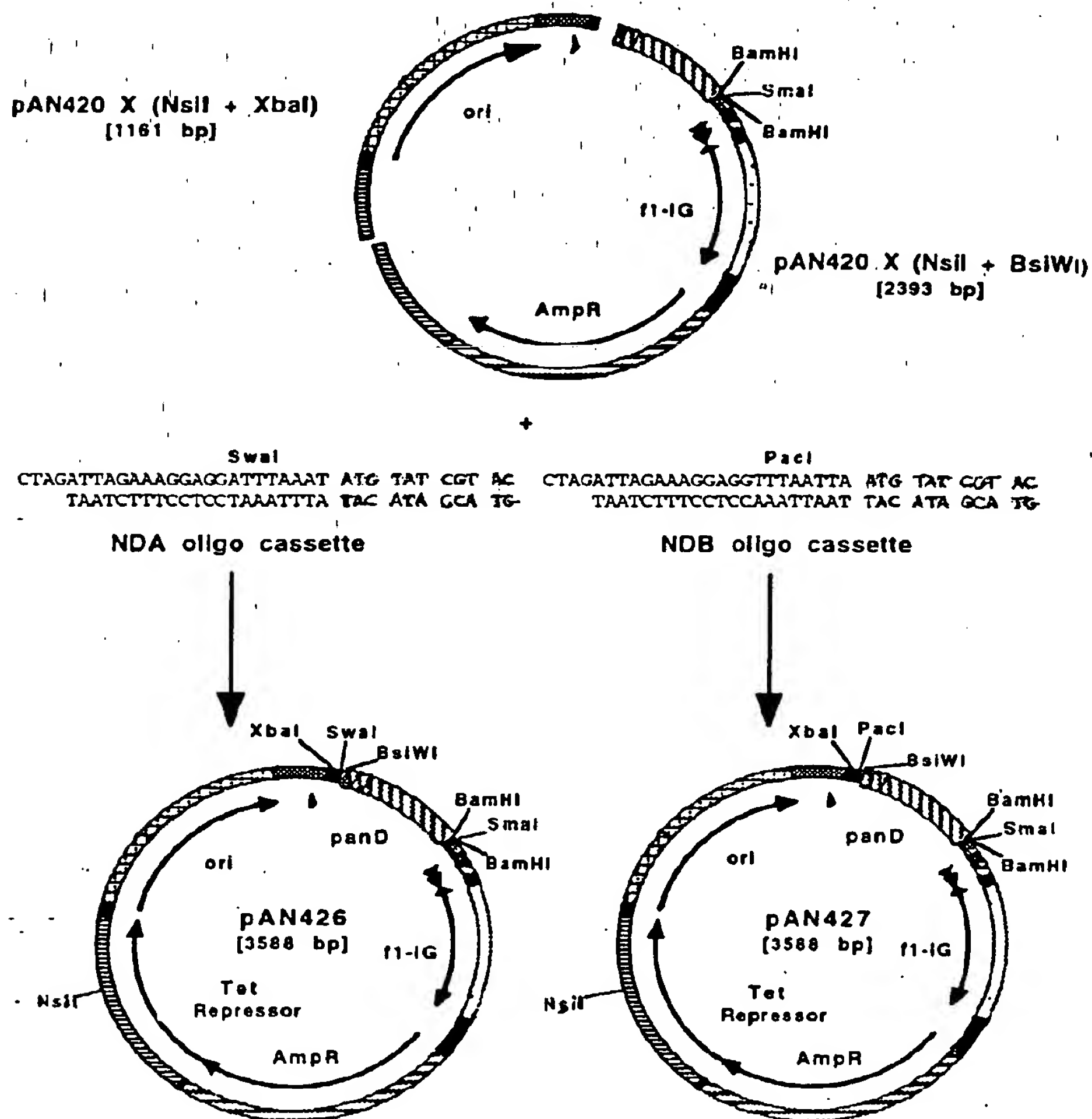


Figure 7 Construction of pAN428 and pAN429.

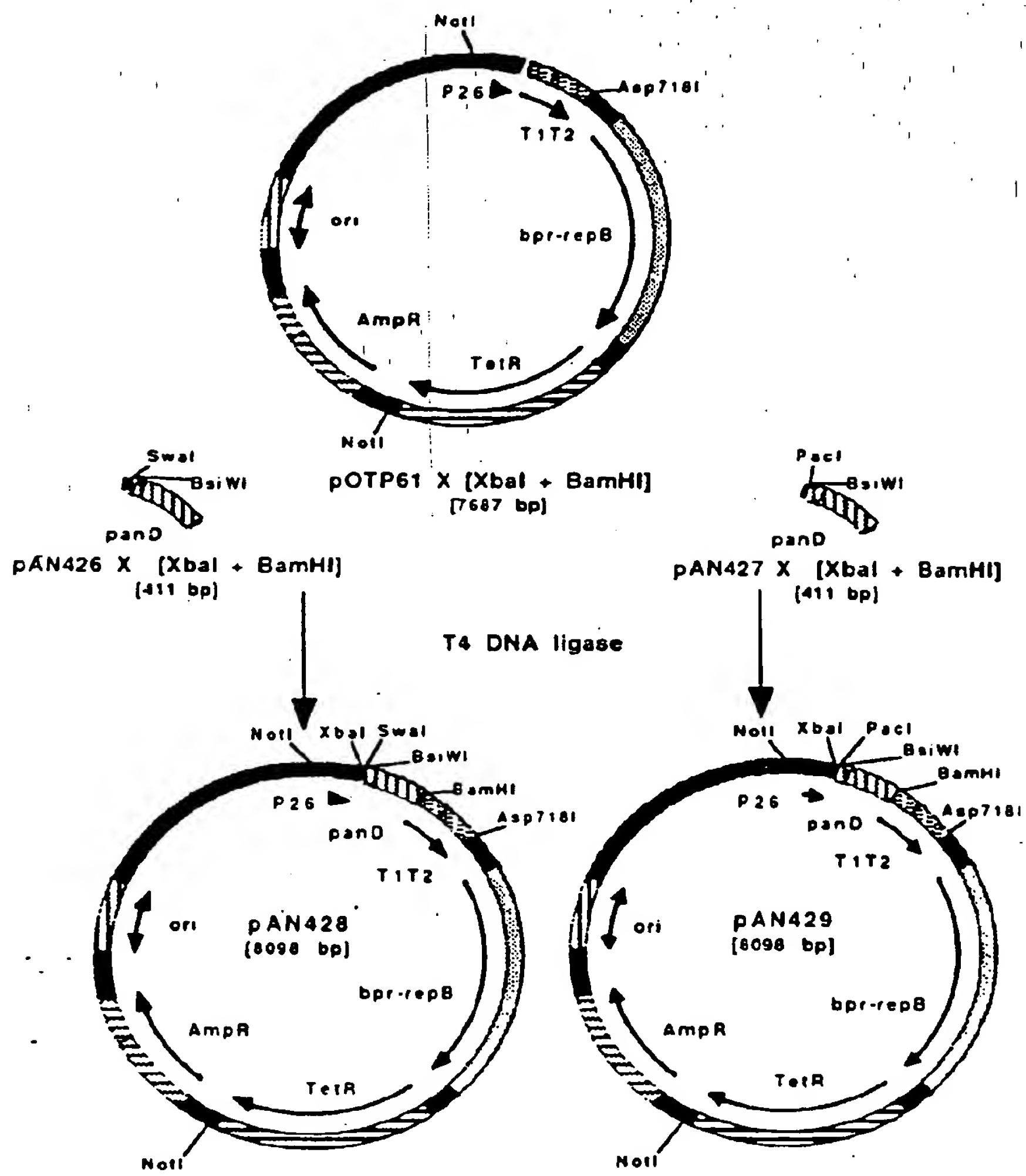


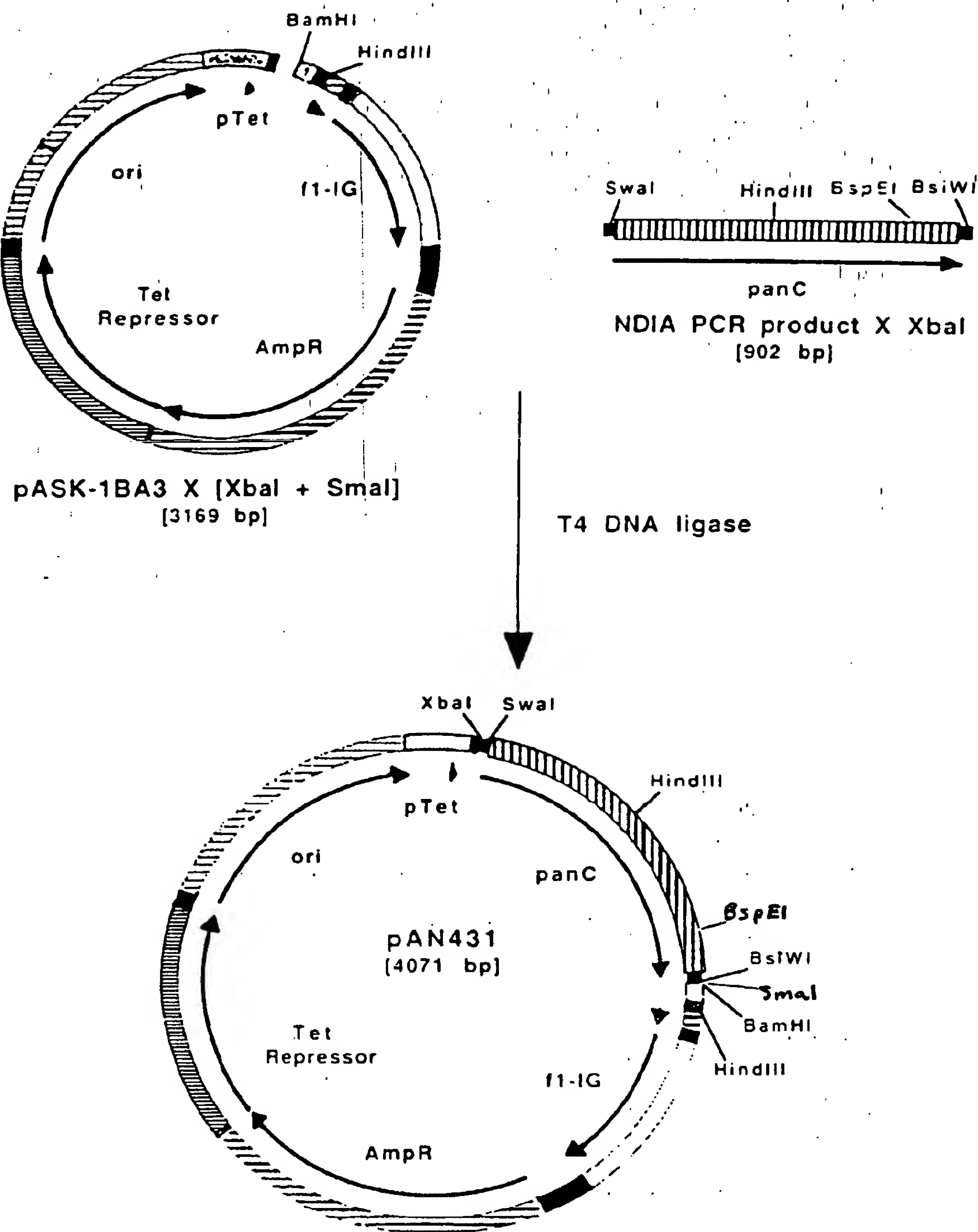
Figure 8. Construction of pAN431.

Figure 9. Construction of pAN441.

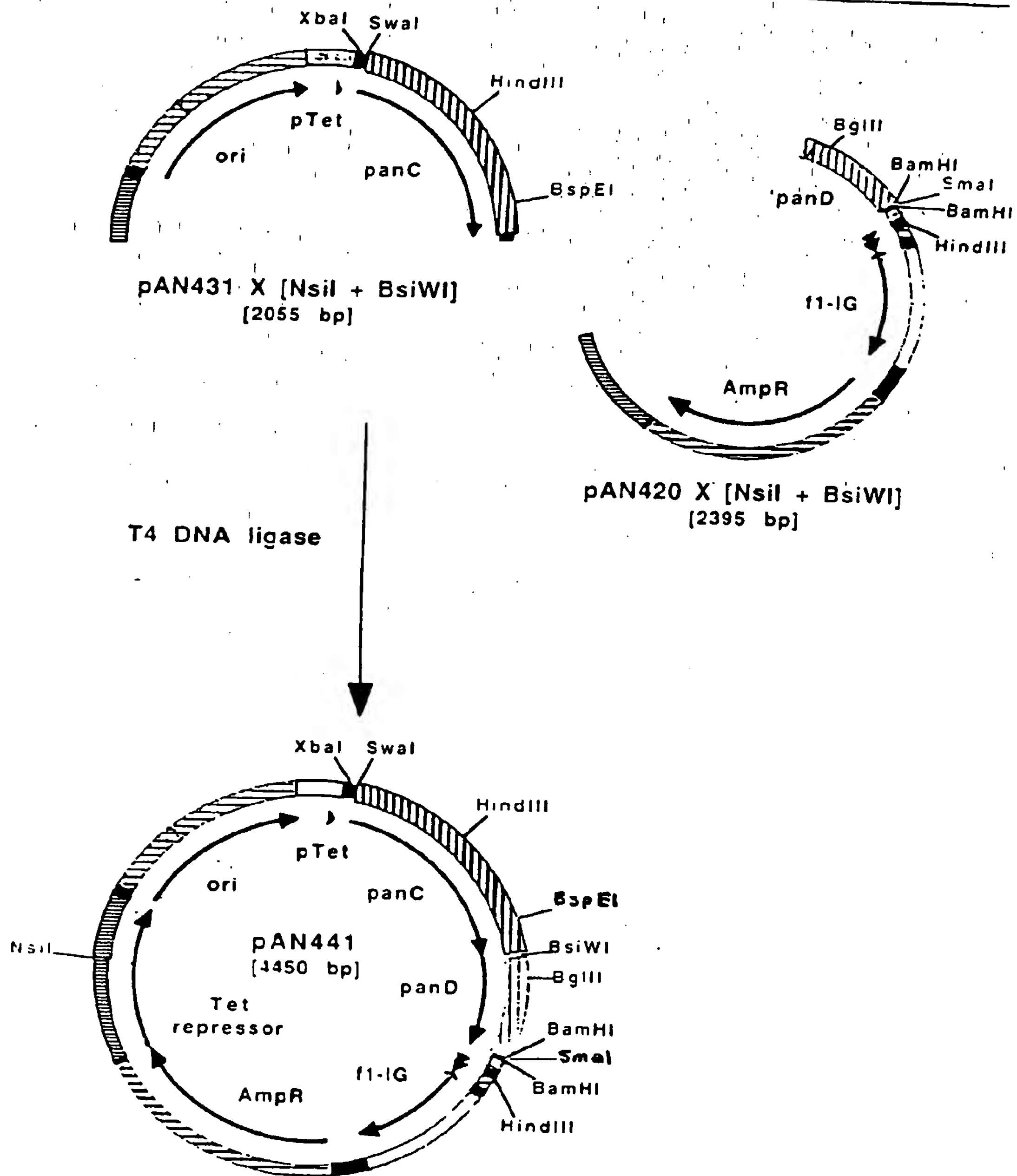
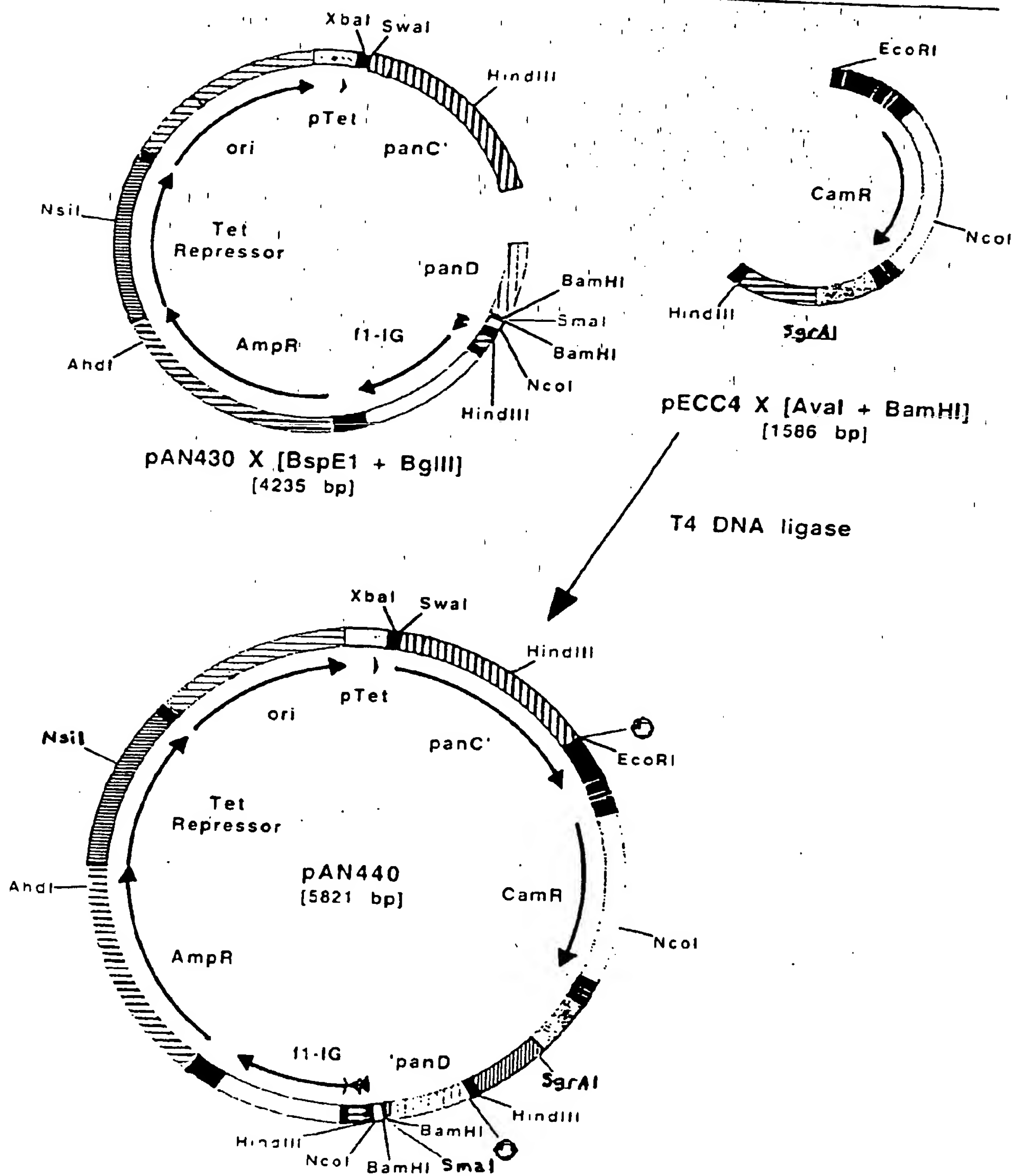


Figure 10. Construction of pAN440.



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Figure 1| Structure of pAN251, a plasmid designed to integrate a single copy of P₂₆ panE1 at the panE1 locus by double crossover.

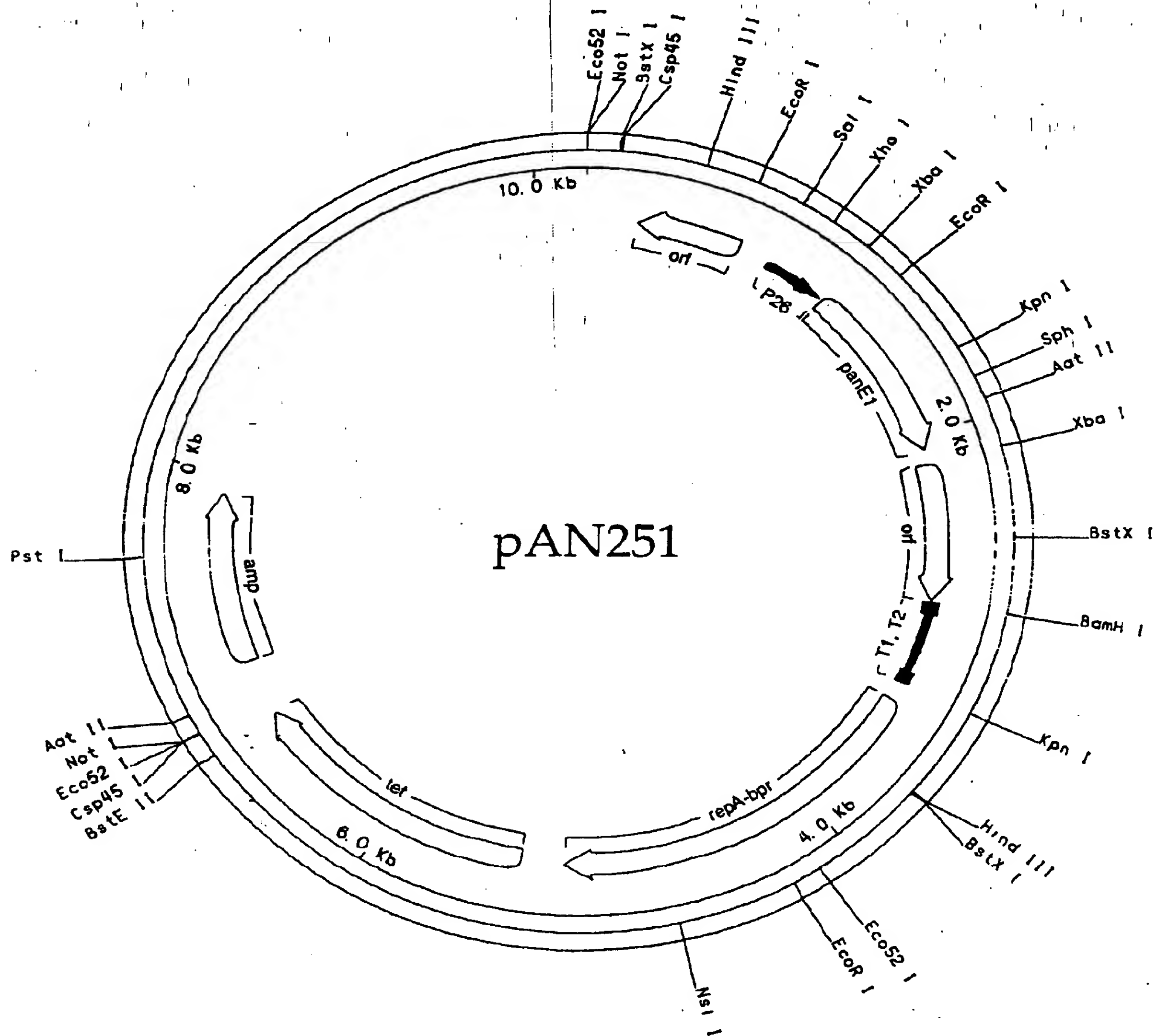


Figure 12 Structure of pAN267, a plasmid designed to stably integrate a P₂₆ ilvBNC cassette at the amyE locus.

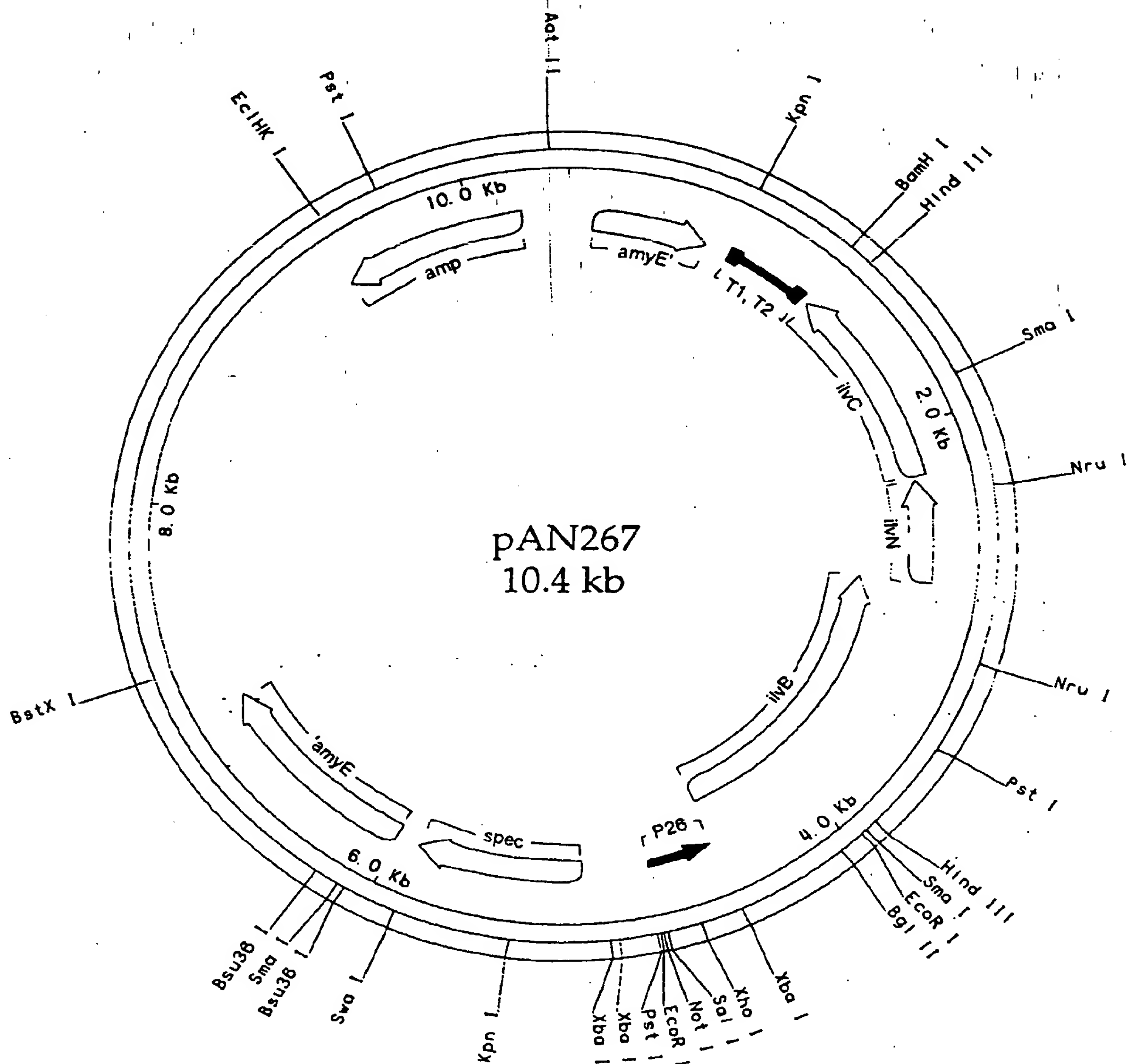


Figure 13 Structure of pAN257, a clone of *B. subtilis* *ilvD* in a low copy vector.

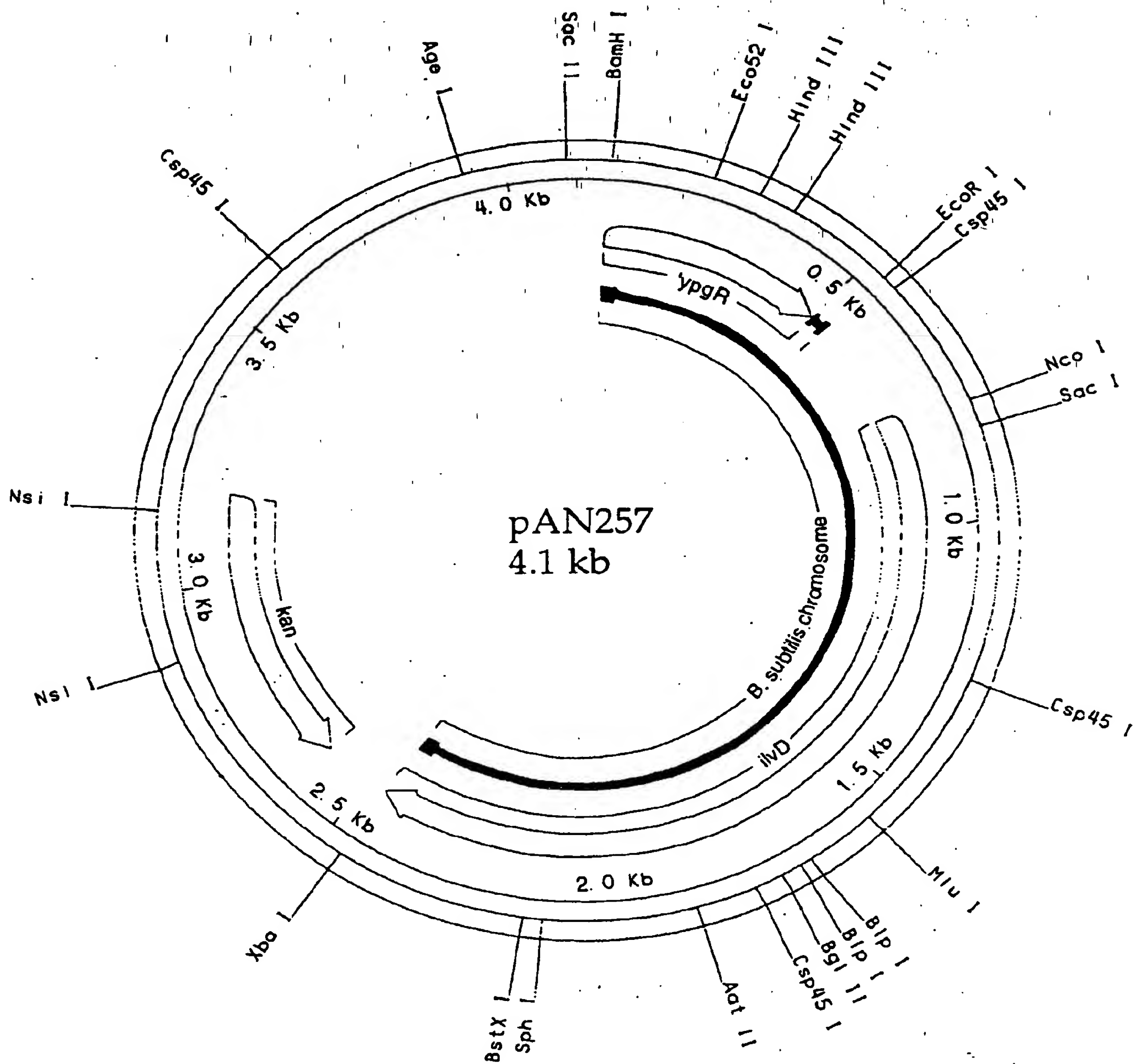


Figure 14 Structure of pAN263, designed to stably integrate a single copy of P₂₆ ilvD at the ilvD locus.

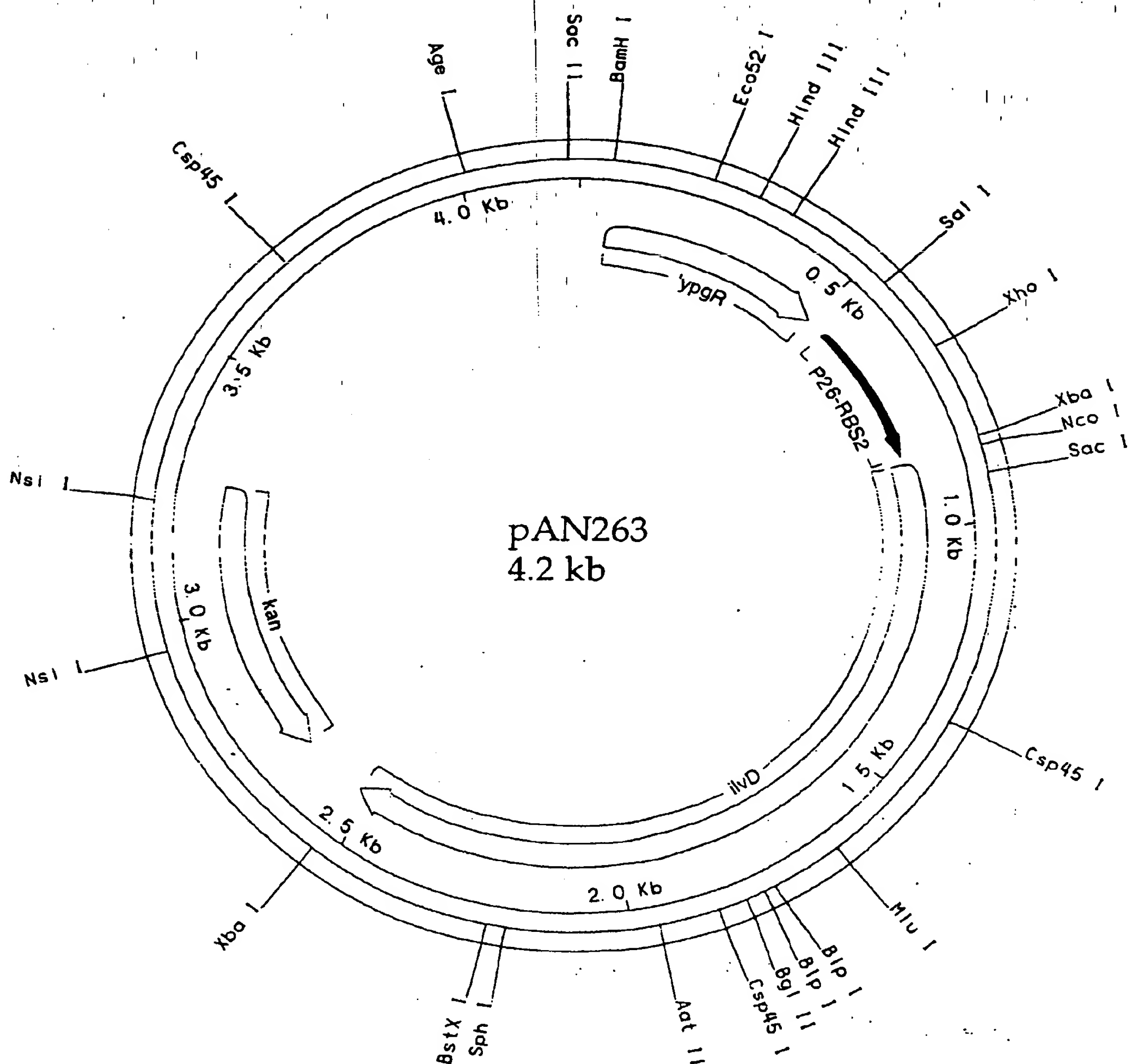


Figure 15 Structure of pAN261, designed to disrupt the *B. subtilis* *ilvD* gene with the *cat* gene.

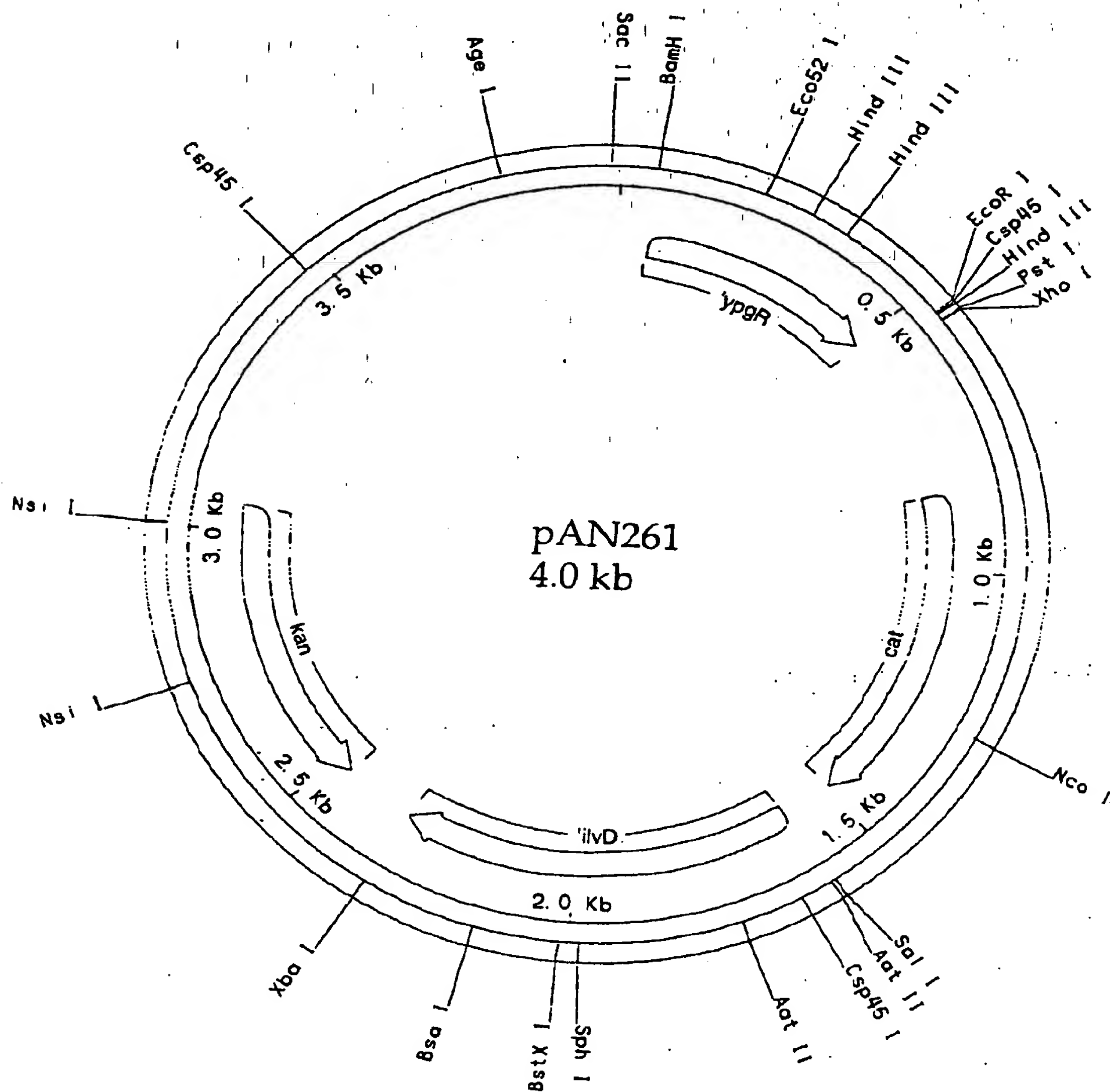


Figure 16

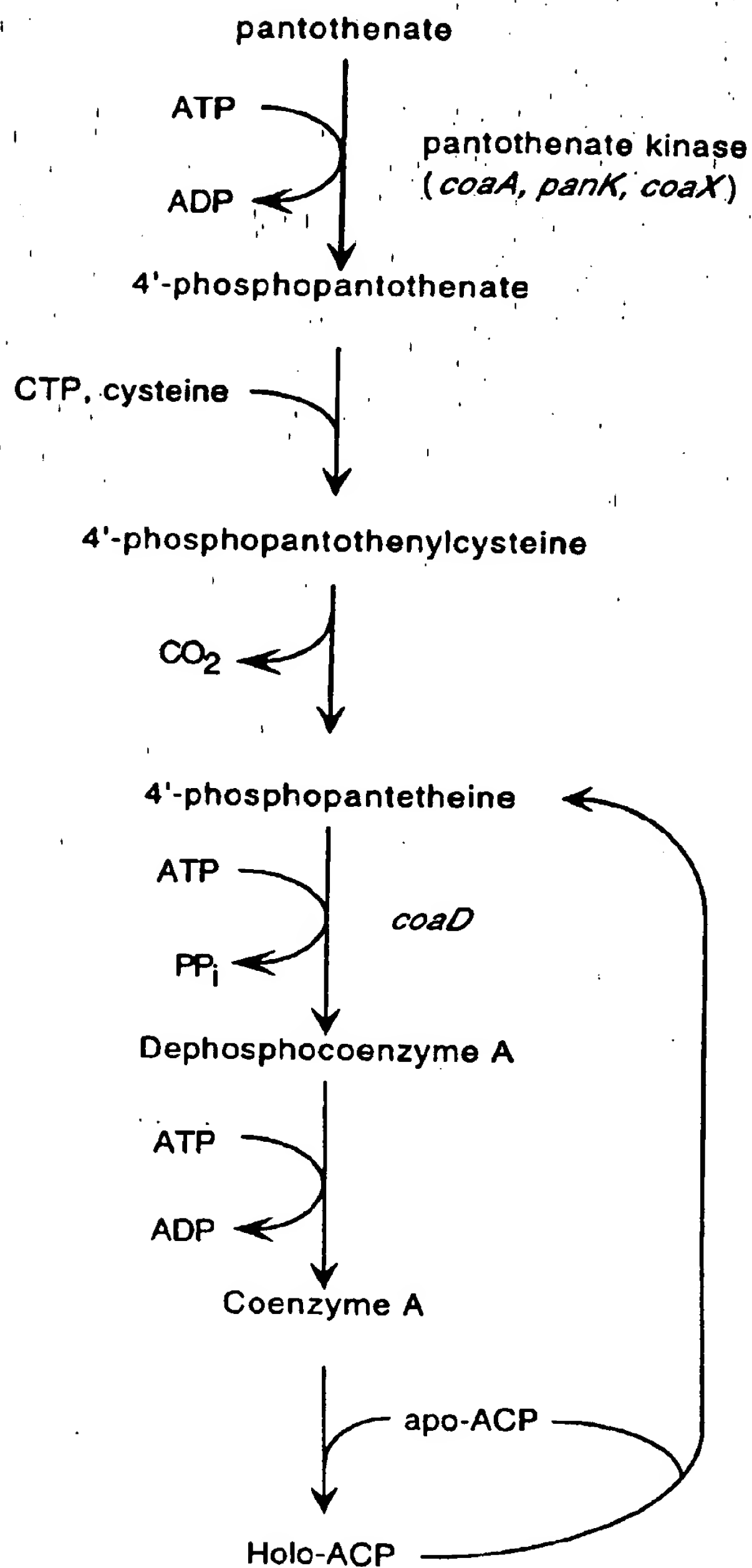


Figure 17 Structure of pAN296, designed to delete most of the *B. subtilis* *coaA* gene and substitute a chloramphenicol resistance gene.

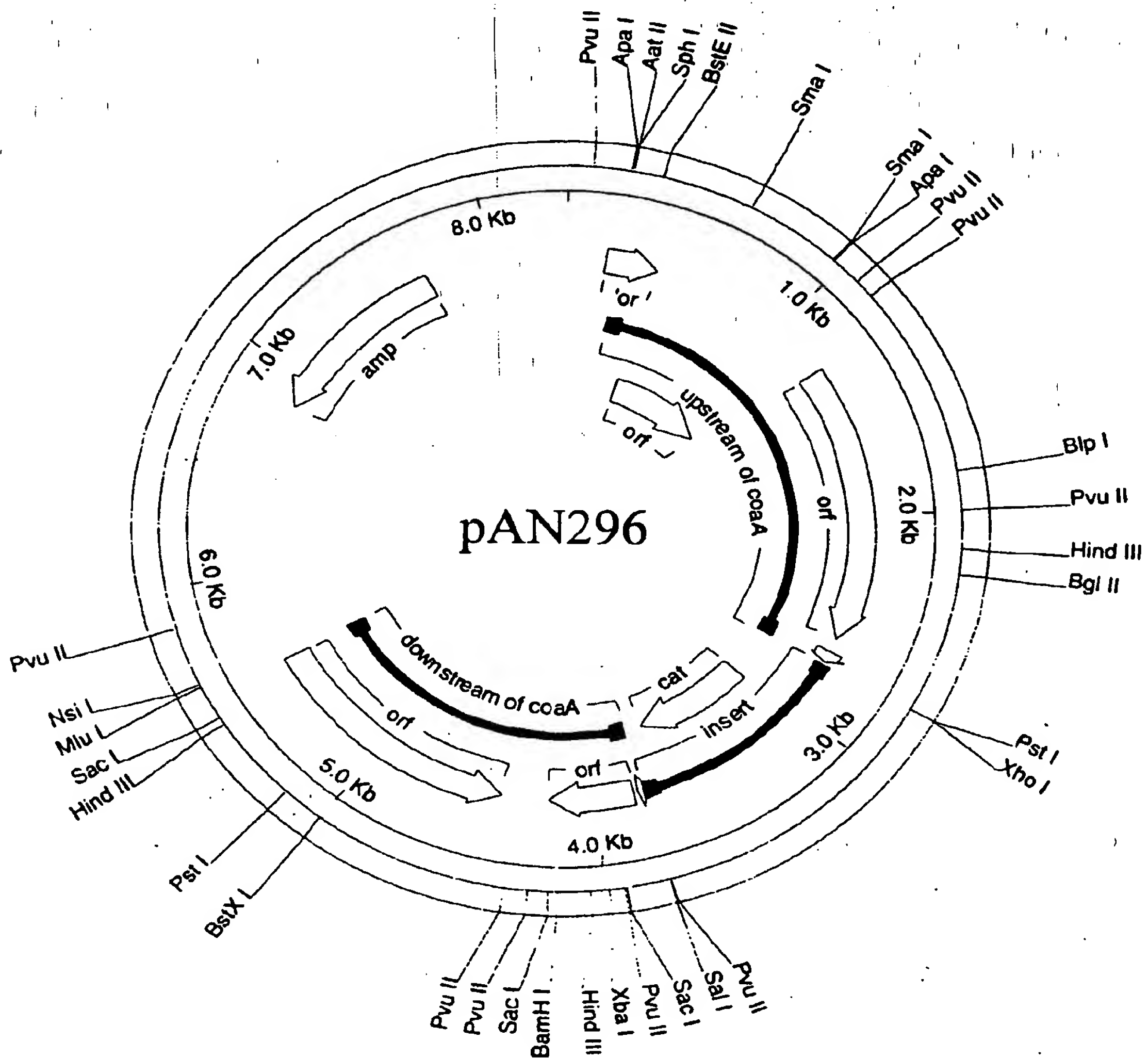


Figure 3 Structure of the B. subtilis chromosome in the region of the coaA gene. The scale is in base pairs and the significant open reading frames are shown by the open arrows.

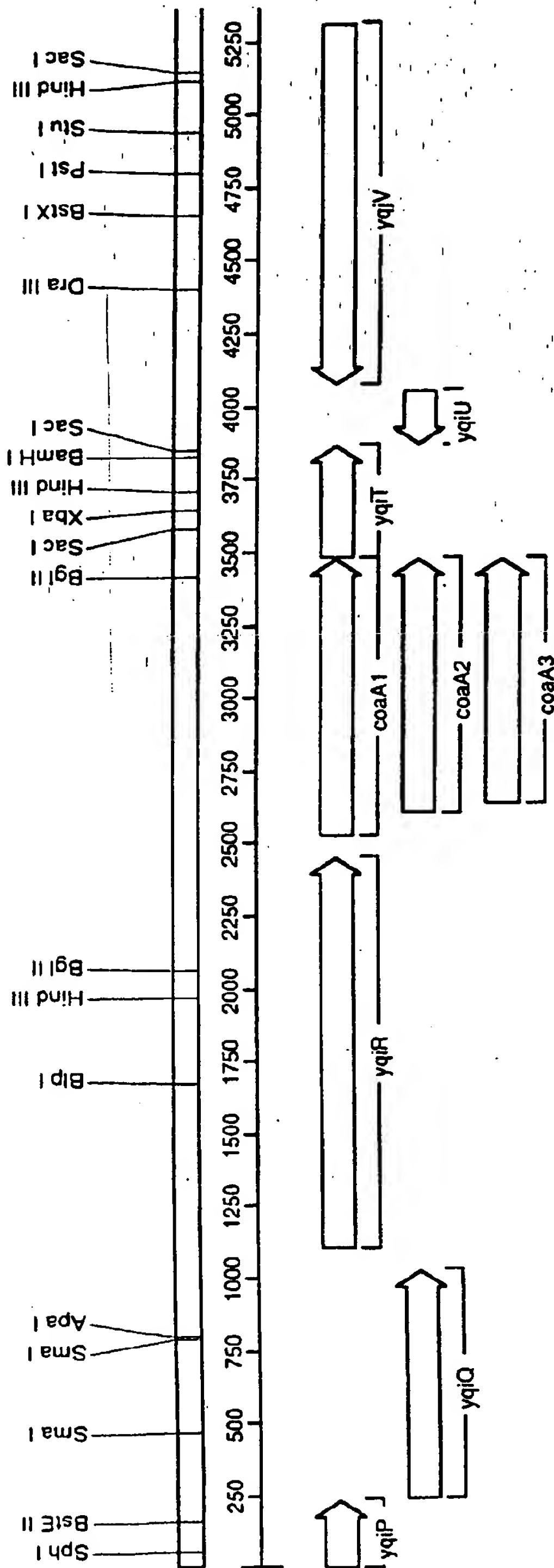
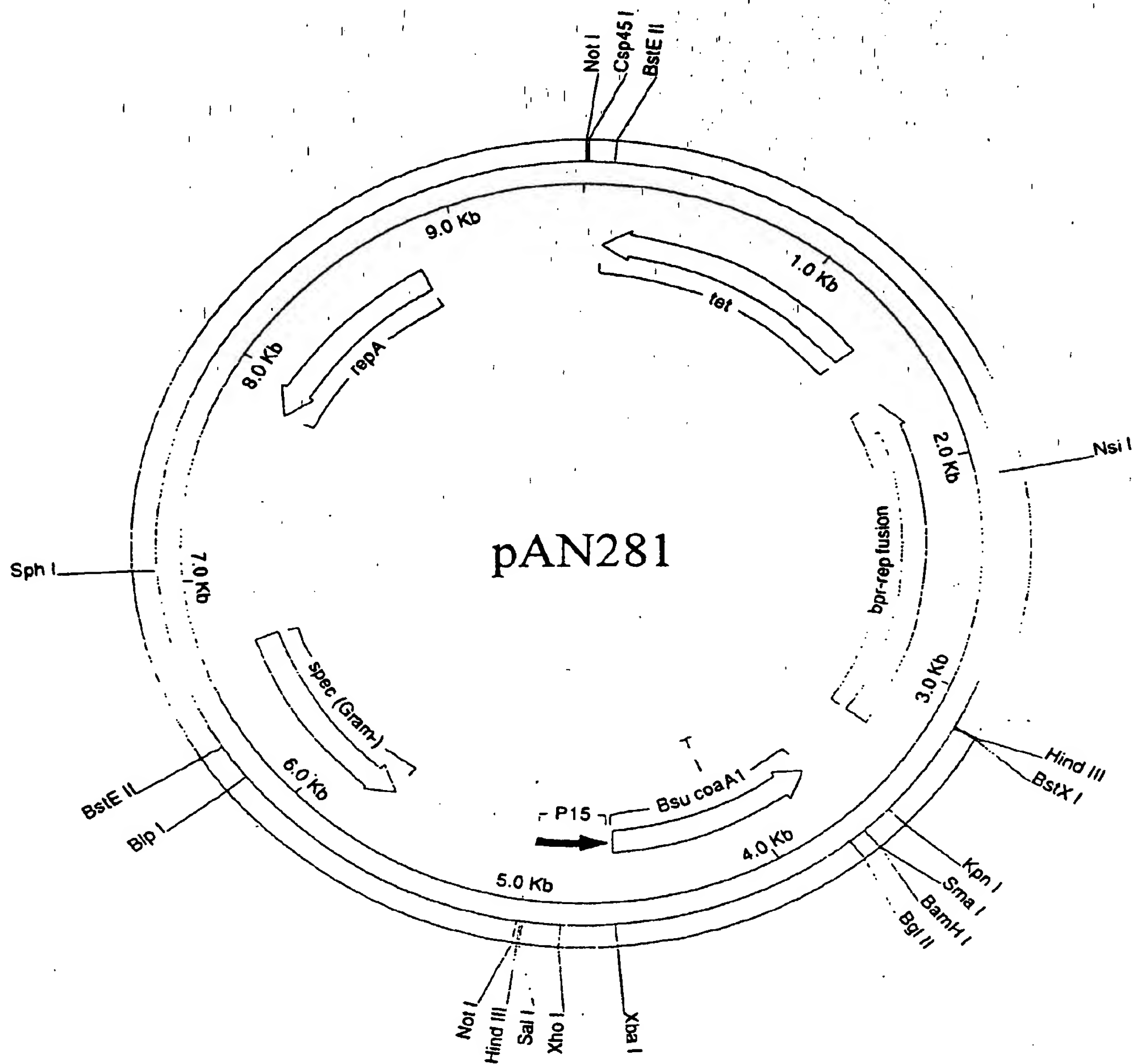


Figure 19. Structure of pAN281, a plasmid for expressing *B. subtilis* *coaA* after integration at the *bpr* locus. pAN282 and pAN283 have similar structures.



CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence type explicitly set to Protein

Sequence format is Pearson

Sequence 1: sp|Q9X795|M.leprae 312 aa

Sequence 2: [sp|086779|S.coelicolor](#) 329 aa

Sequence 3: sp|053440|M.tuberculosis 312 aa

Sequence 4: sp|P54556|B.subtilis 319 aa

Sequence 5: sp|P44793|H.influenzae 311 aa

Sequence 6: sp|P15044|E.coli 316 aa

sp|Q9X795|M.leprae
sp|O53440|M.tuberculosis
sp|O86779|S.coelicolor
sp|P44793|H.influenzae
sp|P15044|E.coli
sp|P54556|B.subtilis

sp|Q9X795|M.leprae
sp|O53440|M.tuberculosis
sp|O86779|S.coelicolor
sp|P44793|H.influenzae
sp|P15044|E.coli
sp|P54556|B.subtilis

sp|Q9X795|M.leprae
sp|O53440|M.tuberculosis
sp|O86779|S.coelicolor
sp|P44793|H.influenzae
sp|P15044|E.coli
sp|P54556|B.subtilis

FIG.20B

sp|Q9X795|M.leprae
sp|O53440|M.tuberculosis
sp|O86779|S.coelicolor
sp|P44793|H.influenzae
sp|P15044|E.coli
sp|P54556|B.subtilis

GRRNLMHRKGFPESYNRRALMRFTSVKSGADYACAPVYSHLRYDTIPGA
QRRNLMHRKGFPESYNRRALMRFTSVKSGSDYACAPVYSHLHYDIIPGA
EARGLMSRKGFPESYDRRALTRFVADIKAGKAETAPVYSHLIYDIPDQ
KQDNLLQKKGFPSYDTPKLIREFLADVKGKSNVTAPIYSHLTYDIIPDK
KERGLMKKGFPESYDMHRLVKFVSDLKSGVPNTAPVYSHLIYDVIPDG
KKKNMMSRKGFPESYDVKALJEFNLNLSKSDSVKAPVYSHLTYDREEGV
* : : **** * : : * : : * : : * : : * : : * : : *

sp|Q9X795|M.leprae
sp|O53440|M.tuberculosis
sp|O86779|S.coelicolor
sp|P44793|H.influenzae
sp|P15044|E.coli
sp|P54556|B.subtilis

KHVVRHPDILILEGLNVLTGP-----TLMVSDLDFSLYVDARIQD
EQVVRHPDILILEGLNVLTGP-----TLMVSDLDFSLYVDARIED
RLVVRRPDILIVEGLNVLPALPGKDGRTRVGLADYDFDSYVVDARTED
FDVVDKPDILILEGLNVLTGNK---TD-QTEVSDFVDFSIYVDAEEKL
DKTVVQPDILILEGLNVLSGMDYPHDPH-HVFVSDVDFVDFSIYVDAPEDL
FEVVEQADIVIIIEGINVLQPTLEDDRENPRIFVSDFEFDFSIYVDAEESR
* : : *** : *

sp|Q9X795|M.leprae
sp|O53440|M.tuberculosis
sp|O86779|S.coelicolor
sp|P44793|H.influenzae
sp|P15044|E.coli
sp|P54556|B.subtilis

IEQWYVSRFLAMRGTAFAFPESHFHHYSALTDSKAIIAAREIWRISNRPN
IEQWYVSRFLAMRTTAFADPESHFHHYAAFSDSQAVVAAREIWRITNRPN
IERWYLNRFKRLRATAFQNPSSYFRKYTVSEEEALDYARTTWRTINKPN
LKWYIKRELKERESAFNDPNSYFKHYASLSKEEAATASKIWDINGLN
LQTWYINRFLKREGAFTDPDSYFHNYSKLTKEEAIKTAMTLWKEINWLN
IFTWYLERFRLLRETAFAQNPDSYFHKFKDLSQDEADMAASIWESVNRPN
* : : *** : : * : : * : : * : : * : : * : : * : : *

sp|Q9X795|M.leprae
sp|O53440|M.tuberculosis
sp|O86779|S.coelicolor
sp|P44793|H.influenzae
sp|P15044|E.coli
sp|P54556|B.subtilis

LVENILPTRPRATLVLRKDADHSINRLRLRKL
LVENILPTRPRATLVLRKDADHSINRLRLRKL
LVENVAPTRGRATLVLRKGPDKVQRLSLRKL
LNQNILPTRERANLILKKGHNHQLVLIKLRK-
LKQNILPTRERASLILTKSANHAEEVRLRK-
LYENILPTKFRSDLILRKGDGHHKVEEVLVRRV
* : : *** : : * : : * : : * : : * : : * : : * : : *

Figure 21

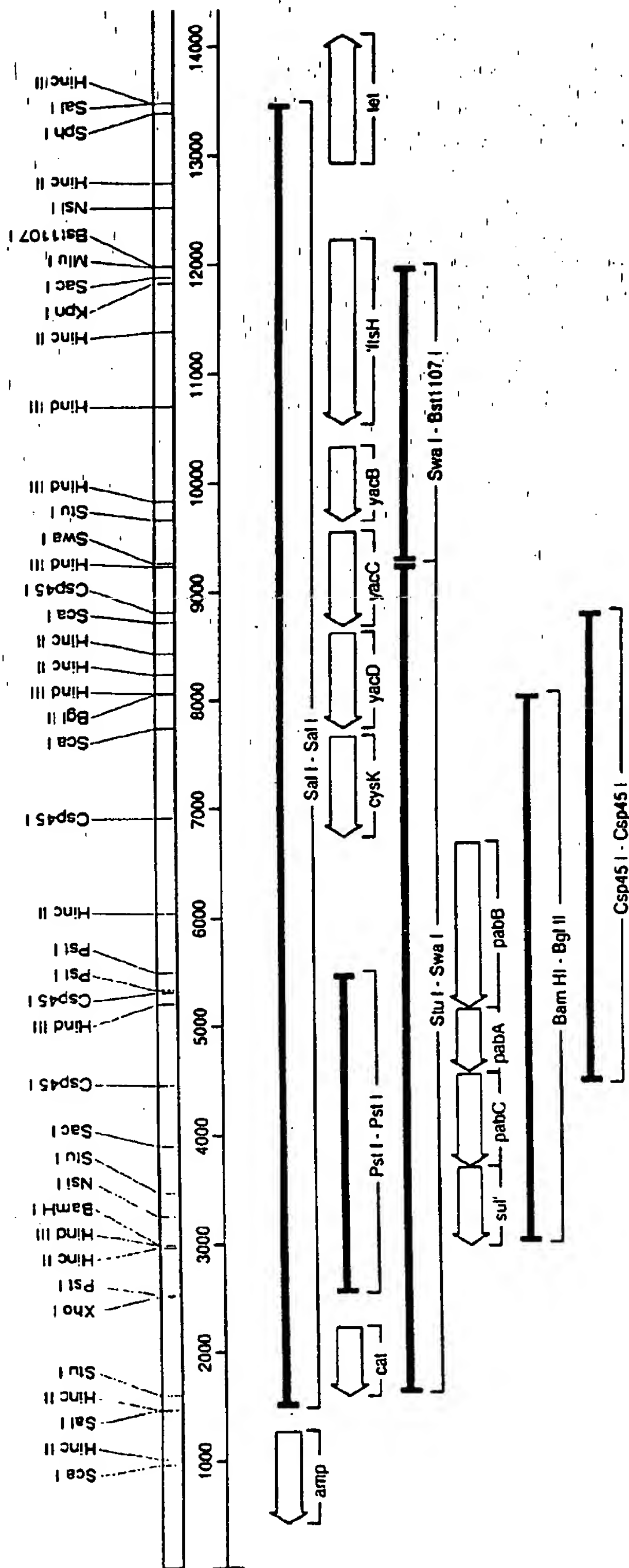


Figure 22 Structure of pAN341 and pAN342, two independent PCR-derived clones of *yacB* (renamed *coaX*).

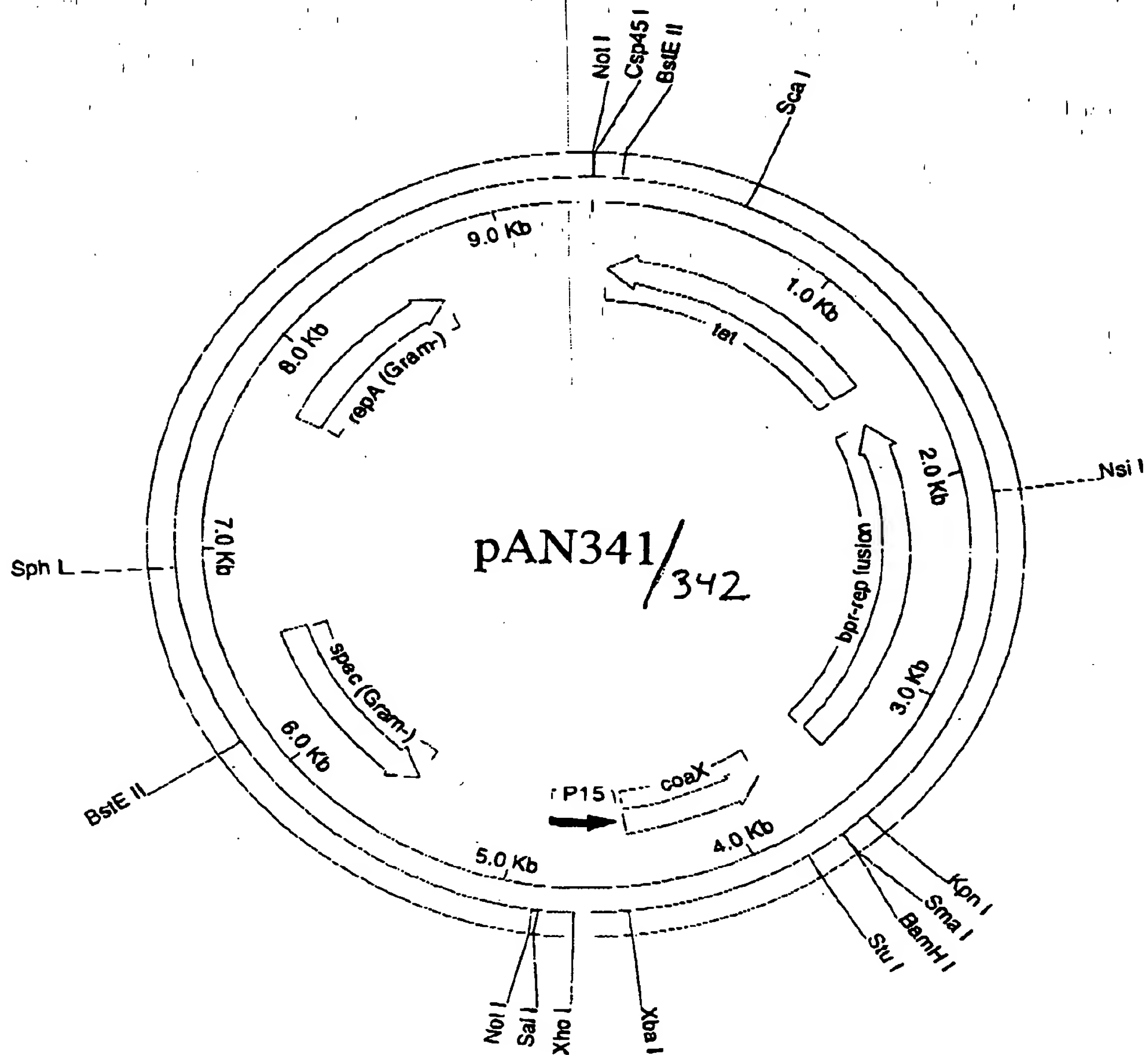


FIG.23A

CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence type explicitly set to Protein

Sequence format is Pearson

Seq. 1: B.subtilis Coax SEQNO_9	258 aa	Seq. 8: sp O51477 B.burgdorferi	262 aa
Seq. 2: dbj BAA21476.1 D.vulgaris	212 aa	Seq. 9: sp P74045 Synechocystis	257 aa
Seq. 3: gb AAD35964.1 T.maritima	246 aa	Seq. 10: sp O25533 H.pylori	223 aa
Seq. 4: pir T36391 S.coelicolor	265 aa	Seq. 11: sp O67753 A.aeolicus	229 aa
Seq. 5: sp Q45338 B.pertussis	267 aa	Seq. 12: sp Q9RX54 D.radiodurans	262 aa
Seq. 6: sp O06282 M.tuberculosis	272 aa	Seq. 13: WIT RCA03301 C.acetobutylicum	250 aa
Seq. 7: sp O83446 T.pallidum	273 aa	Seq. 14: WIT RR02473 R.capsulatus	258 aa

B.subtilis Coax SEQIDNO_9	-----MLLVIDVGNTNTVLGVYHDG-----KLEYHWRIE
WIT RCA03301 C.acetobutylicum	NKRAAFMLLLFLRSVLKVLVLDVGNTNIVLGIYNDT-----KLTAEWRLS
pir T36391 S.coelicolor	-----MLLTIDVGNTHTVLGLFDGE-----DIVEHWRI
sp O06282 M.tuberculosis	-----MLLAIDVRNTHTVVGLLSGMKEHAKVVQWRIR
WIT RR02473 R.capsulatus	-----MLLCIDCGNTNTVFSVWDGT-----DFAATWRIA
dbj BAA21476.1 D.vulgaris	-----MTQHFLLEDIGNTNVKIGIAVET-----AVLTSYVLP
sp Q9RX54 D.radiodurans	-----MPAFPLLAVDIGNTTTVLGLADASG-----ALHTWRI
gb AAD35964.1 T.maritima	-----MYLLVDVGNTHTSVFSITEDG-----KTFRRWRLS
sp O83446 T.pallidum	-----MLLIDVGNSHVVFQIQGNGGRCVRELFRLA
sp O51477 B.burgdorferi	-----MNKPLLSELIIDIGNTSIAFALFKDN-----QVNLFIKMK
sp O67753 A.aeolicus	-----MRELTVDVGNSVDIALWEGK-----KVK
sp P74045 Synechocystis	-----METSKECCGLALDNDKQKPLWGLMIGN-----SRLHWAYC
sp O25533 H.pylori	-----MPARQSFDTLKN-----LVLCDIGN-----TR
sp Q45338 B.pertussis	-----MIILIDSGNSRLKVGWFDPDAP---QAAREPAPV

FIG.23B

B.subtilis Coax SEQIDNO_9	TSRHKTEDEFGMILRSLFDHS-----GLMFEQIDGIIISSVVPPIMFALER
WIT RCA03301 C.acetobutylicum	TDVLSADEYGIQVMNLFQOD-----KLDPTLVEGVIISSVVPNIMYSLEH
pir T36391 S.coelicolor	TDSRRTADELAVLLQGLMGHPLLGDELGDIDGIAICATVPSVLHELRE
sp O06282 M.tuberculosis	TESEVTADELALTIDGLIG-----EDSERLTGTAALSTVPSVLHEVRI
WIT RRC02473 R.capsulatus	TDHRRTADEYFVWLNTLMQLK-----GLQGRISEAIISSAPRVVFNLRV
dbj BAA21476.1 D.vulgaris	TDPGQTTDSIGRLLEVLRHAG-----LGPADVGCACVASSVVPVGNPLIRR
sp Q9RX54 D.radiodurans	TNREMLPDDLALQLHGLFTLA-----GAP-IPRAAVLSSVAPPVGENYAL
gb AAD35964.1 T.maritima	TGVFQTEDELFSLHPLLG-----DAMREIKGIGVASVVPVPTQNTVIER
sp O83446 T.pallidum	PDARKTQDEYSLLIHALCERAG-----VGRASLRDAFISSVVPVLTTKTIAD
sp O51477 B.burgdorferi	TNMLRYDEVYSFTEENFDEN-----VN---K-VFISSVVPILNETFKN
sp O67753 A.aeolicus	DFLKL SHEEFLEEFPKLK-----ALGISVKQSFSEKVRG
sp P74045 Synecocystis	SGNAPLQTWVTDYNPKSAQLP-----VLLGKVPLMLASVVPE
sp O25533 H.pylori	IHFAQNYQLFSSAKEDLKR-----LGIQKEIFYISVNEE
sp Q45338 B.pertussis	AFDNLDLDALGRWLATLPRRP-----Q-----RALGVNVAGLARGEAIA
B.subtilis Coax SEQIDNO_9	MCTKYFHI EQIVG-PG-MKTGLN IKYDNPKEVGADRIVNAVA AIHLYG-
WIT RCA03301 C.acetobutylicum	MIRKYEKINPLVVG-PG-IKTGINIKYDNPKEVGADRIVNAVA AHEIYK-
pir T36391 S.coelicolor	VTRRYG DVP AVLVEPG-VKTGVPILTDHPKEVGADRIINAVAAVELYG-
sp O06282 M.tuberculosis	MLDQYWPSPVHVLIEPG-VRTGIPLLVDNPKKEVGADRIVNCLAA YDRFR-
WIT RRC02473 R.capsulatus	LCNRYFDCRPYVVGKPG-CELPVAPRVDPGTTVGPDRLVNTVAGYDRHG-
dbj BAA21476.1 D.vulgaris	ACERYL--YRKL LFAPGDIAIPLDNRYERPAEVGADRLVAAYAA RRLYP-
sp Q9RX54 D.radiodurans	ALKRHEMIDAFVSAEN--LPDVTVELDTPGSVGADRLCNLFGAEKYL G-
gb AAD35964.1 T.maritima	FSQKYFHI SPIWVAKN---GCVKWNVKNPSEVGADRVANVVA FVKEYG-
sp O83446 T.pallidum	AVAQISGVQPVVFGPWAYEHLPVRIPEPVRAEIGTDLVANAVAA YVHER-
sp O51477 B.burgdorferi	VIFSEFKIKPLFIFGDLN YDLTENPYKSKDFLLGSDVFANLVAAIENYS-
sp O67753 A.aeolicus	KIPKIK-----FLKKEN---FPIQVDYKTPETLTGTD RVALAYS AKKFYG-
sp P74045 Synecocystis	QTEVWRVYQPKILT LKN---LPLVNLYP---SFGIDRALAGLGTGLTYG-
sp O25533 H.pylori	NEKALLNCYPNAKN IAG--FFHLETDYVG---LGIDRQMACLA---VN--
sp Q45338 B.pertussis	ATLRAGGCDIRWLRAQP-LAMGLRNGYRNPDLGADRWACMVGV LARQPS

FIG.23C

B. subtilis Coax SEQIDNO_9	NP--LIVVDFGTATTYCYIDENKQYMGGAIAPIGITISTEALYSRAAKLPR
WIT RCA03301 C.acetobutylicum	RS--LIIIDFGTATTFCAVRENGDYLGGAIICPGIKVSSSEALFEKAAKLPR
pir T36391 S.coelicolor	GP--AIVVDFGTATTFDAVSARGEYIGGVIAPGIEISVEALGVKGAQLRK
sp O06282 M.tuberculosis	KA--AIVVDFGSSICVDVVSAGKEFLGGAIAAPGVQVSSDAAAARSALRR
WIT RR02473 R.capsulatus	GD--LIVVDFGTATTFDVVAPDGAYIGGVIAPGVNLSLEALHMAAALPH
dbj BAA21476.1 D.vulgaris	GPRSLVSVDFGTATTFDCVEG-GAYLGGILCPGVLSAGALSSRTAKLPR
sp Q9RX54 D.radiodurans	GLDYAVVDFGTSTNFDVVGRRRFLGGILATGAQVSADALFARAANKLPR
gb AAD35964.1 T.maritima	KN--GIIIDMGATTVDLVVN-GSYEGGAILPGFFMMVHSLFRGTAKLPL
sp O83446 T.pallidum	SA--CVVDCGTALTFTAVDGTGLIQGVAIAPGLRTAVQSLHTGTQQLPL
sp O51477 B.burgdorferi	FEN-VLVOLGTACTIFAVSRQDGLGGIINSGLINFNLSLLDNAYLIK
sp O67753 A.aeolicus	KN--VVVISAGTALVIDLVE-GKFKGGFITLGLGKKILSDLAEGIPE
sp P74045 Synecocystis	EP--CLVVDGGTALTITGFDQDKLVGGAILPGLGLQATLGDRLAALPK
sp O25533 H.pylori	NG---VVVDAGSAITIDLIKE-GKHLGGCILPGLAQYIHAYKKSAKILEQ
sp Q45338 B.pertussis	VHPPLLVSFGTATTLDITGPDNVFPGGLILPGPAMMRGALAYGTAHLPL
	: . +:: : . + : *
B. subtilis Coax SEQIDNO_9	IEITRPDN---IIGKNTVSAMQSGILFGYVGQVEGIVKRMKWQAKQDLK-
WIT RCA03301 C.acetobutylicum	VELIKPAY---AICKNTISSIQSGIVRYLRQVKYLFKELKENLPDGRRT
pir T36391 S.coelicolor	IEVARPRS---VIGKNTVEAMQSGIVYGFAGQVDGVNRMARELADD--P
sp O06282 M.tuberculosis	VELARPRS---VVGKNTVECMQAGAVFGEAGLVGDLVGRIRREDVSGFSVD
WIT RR02473 R.capsulatus	VDVTKPQG---VIGTNTVACIQSGVYWGVIIGLVEGIVRQIRMERDRP---
dbj BAA21476.1 D.vulgaris	ISLEVEEDS-PVIGRSTTSLNHGFIFFGAAMTEGVLA--
sp Q9RX54 D.radiodurans	ITLQAPET---AIGKNTVHALQSGLVFGYAEMVDGLLRIRRAELPGE---
gb AAD35964.1 T.maritima	VEVKPAOF---VVGKDEENIRLGVVNGSVYALEGIIIGRIKEVYGDLP---
sp O83446 T.pallidum	VPLALPDS---VLGKDTTHAVQAGVVRGTLFVIRAMIAQCQKELGCR---
sp O51477 B.burgdorferi	FPISTPNN---LLERTTSGSVNSGLFYQYKYLIEGVYRDIKQMYKKK---
sp O67753 A.aeolicus	FFPEEVEI---FLGRSTRECVLGGAYRESTEFIKSTLKLWRKVFKRK---
sp P74045 Synecocystis	LEMDQLTELPDRWALDTPSAIFSGVVYGVLGALQSYLQDWQKLFPGA---
sp O25533 H.pylori	PFKALDSL---EVLPEKSTRDAVNVMVLSVIACTIQLAK--NQK-----
sp Q45338 B.pertussis	ADGLVADY-----PIDTHQAIASGIAAAQAGAIVRQWLGRQRYGQAP---
	* : . +

FIG.23D

B. subtilis Coax SEQIDNO_9	-----VIATGG-----LAPLIANES-----DCIDIVDPFLTLKGLELI
WIT RCA03301 C.acetobutylicum	RTSLVLATGG-----LAKLIN-----
pir T36391 S.coelicolor	DDVTVIATGG-----LAPMVLGES-----SVIDEHEPWLTLMGLRLV
sp O06282 M.tuberculosis	HDVAIVATGH-----TAPLLLPEL-----HTVDHYDQHLTLOGLRLV
WIT RR02473 R.capsulatus	--MKVIATGG-----LASLFDLGF-----DLFDKVEDDLTMHGLRLI
dbj BAA21476.1 D.vulgaris	-----
sp Q9RX54 D.radiodurans	--AVAVATGG-----FSRTVQGIC-----QEIOYYDETLTLRGLVEL
gb AAD35964.1 T.maritima	-----VLTGG-----QSKIVK-DM-----IKHEIFDEDLTIKGVYHF
sp O83446 T.pallidum	--CAAVITGG-----LSRLFS-SE-----VDEPPIDAQLTSLGLAHI
sp O51477 B.burgdorferi	--FNLIITGG-----NADLILSLI-----EIEFIFNIHLTVEGVRIL
sp O67753 A.aeolicus	--FKVITGG-----EGKYFS-----KFGIYDPLLVRGMRNL
sp P74045 Synecocystis	---AMVITGG-----DGKILHGELKEHSPNLSVAWDDNLIIFLGMAAI
sp O25533 H.pylori	----IYLCGG-----DAKYLSAFL-----PHSVCKERLVFDGMEIA
sp Q45338 B.pertussis	---EIYVAGGGWPEVRQEAERLLAVTGAAFGATPQPTYLDSPVLDGLAAL
B. subtilis Coax SEQIDNO_9	YERNRVGSV-----
WIT RCA03301 C.acetobutylicum	-----
pir T36391 S.coelicolor	YERNVSRM-----
sp O06282 M.tuberculosis	FERNLEVQRGLKTAR-----
WIT RR02473 R.capsulatus	FDYNKGLGA-----
dbj BAA21476.1 D.vulgaris	-----
sp Q9RX54 D.radiodurans	WASRSEVR-----
gb AAD35964.1 T.maritima	CFGD-----
sp O83446 T.pallidum	ARLVPTSLPPATVSGSSGN
sp O51477 B.burgdorferi	GNSIDFEKFN-----
sp O67753 A.aeolicus	LYLYHRI-----
sp P74045 Synecocystis	HHGDRPIC-----
sp O25533 H.pylori	LKKAGILECK-----
sp Q45338 B.pertussis	AAQCAPTA-----

Figure 24 Alignment of a portion of the amino acid sequences of several known or suspected pantothenate kinases. The residues that are mutated in E. coli coaA15(Ts) and B. subtilis coaA from plasmid pAN282A are indicated below and above the alignment, respectively. The coordinate given in the left margin for the B. subtilis protein refers to the coaA1 open reading frame.

	K	D	N	V	T	A	P	V	Y	S	H	L	I	Y	D	I	I	P	G	A	Majority
168	K	D	S	V	K	A	P	V	Y	S	H	L	T	Y	D	R	E	E	G	V	B. subtilis CoaA1
167	V	P	N	V	T	A	P	V	Y	S	H	L	I	Y	D	V	I	P	D	G	E. coli CoaA
165	K	S	N	V	T	A	P	I	Y	S	H	L	T	Y	D	I	I	P	D	K	H. influenzae CoaA
169	A	D	Y	A	C	A	P	V	Y	S	H	L	R	Y	D	T	I	P	G	A	M. leprae CoaA
169	S	D	Y	A	C	A	P	V	Y	S	H	L	H	Y	D	I	I	P	G	A	M. tuberculosis CoaA
179	K	A	E	V	T	A	P	V	Y	S	H	L	I	Y	D	I	V	P	D	Q	S. coelestis CoaA

Figure 2S Structure of pAN294, a plasmid for integrating mutagenized *B. subtilis* *coaA* at its native locus.

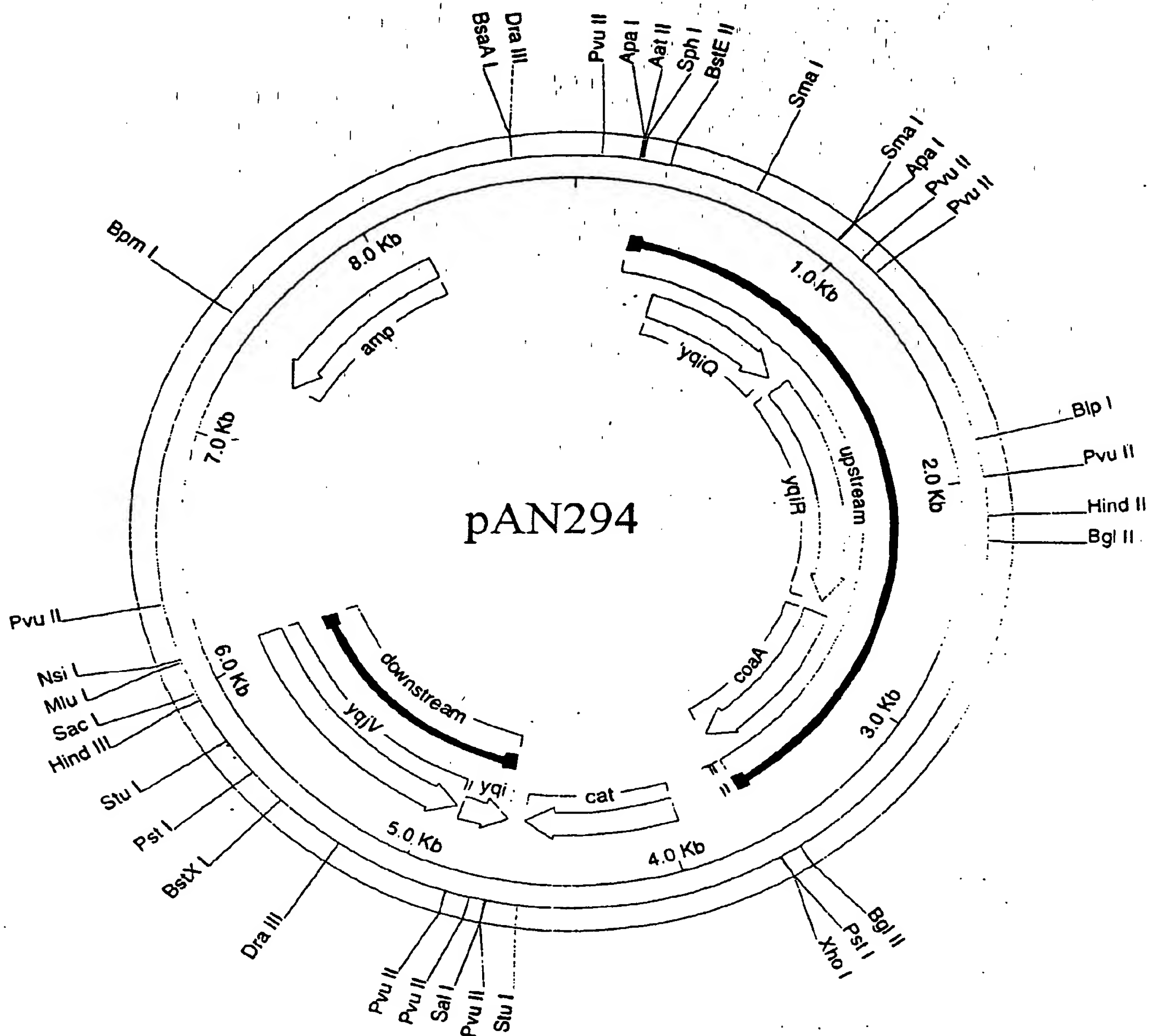
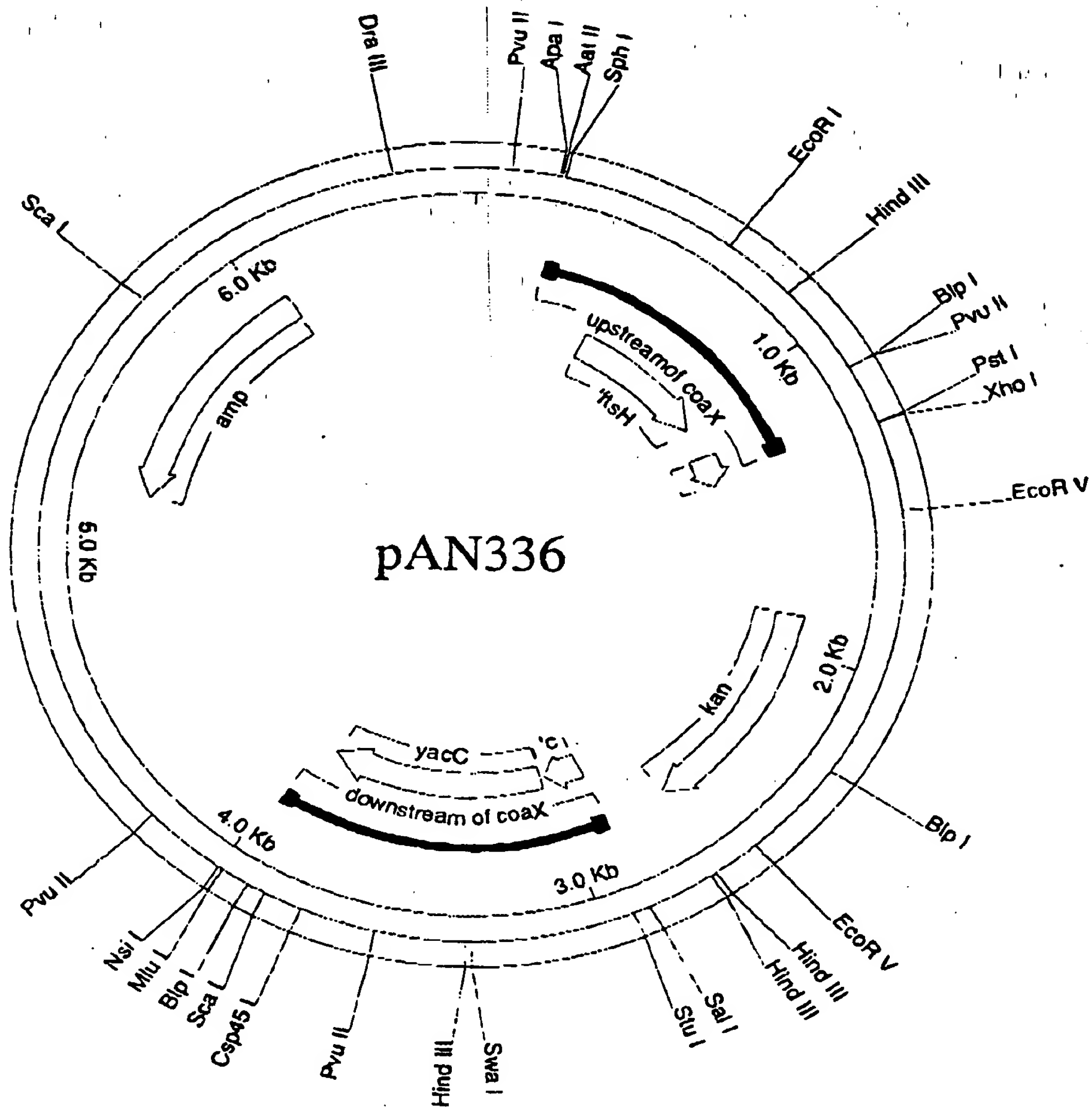


Figure 26 Structure of pAN336, a plasmid designed to delete *B. subtilis* *coaX* from the chromosome and replace it with a kanamycin resistance gene.



- 1 -

SEQUENCE LISTING

<110> OMNIGENE BIOPRODUCTS

<120> METHODS AND MICROORGANISMS FOR PRODUCTION OF
PANTO-COMPOUNDS.

<130> BGI-141CPPC

<140>

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<150> USSN 09/400,494

<151> 1999-09-21

<150> USSN 60/210,072

<151> 2000-06-07

<150> USSN 60/221,836

<151> 2000-07-28

<150> USSN 60/221,836

<151> 2000-08-24

<160> 94

<170> PatentIn Ver. 2.0.

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<211> 311

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<213> Haemophilus influenzae

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Gln	Trp	Ala	Glu	Leu	Arg	Lys	Ser	Val	Pro	Leu	Lys	Leu	Thr	Glu	Gln
		20						25					30		

Asp	Leu	Lys	Pro	Leu	Leu	Gly	Phe	Asn	Glu	Asp	Leu	Ser	Leu	Asp	Glu
		35					40					45			

Val	Ser	Thr	Ile	Tyr	Leu	Pro	Leu	Thr	Arg	Leu	Ile	Asn	Tyr	Tyr	Ile
	50					55					60				

Asp	Glu	Asn	Leu	His	Arg	Gln	Thr	Val	Leu	His	Arg	Phe	Leu	Gly	Arg
	65				70					75					80

Asn	Asn	Ala	Lys	Thr	Pro	Tyr	Ile	Ile	Ser	Ile	Ala	Gly	Ser	Val	Ala
			85						90					95	

Val	Gly	Lys	Ser	Thr	Ser	Ala	Arg	Ile	Leu	Gln	Ser	Leu	Leu	Ser	His
		100						105					110		

Trp	Pro	Thr	Glu	Arg	Lys	Val	Asp	Leu	Ile	Thr	Thr	Asp	Gly	Phe	Leu
		115					120					125			

- 2 -

Tyr Pro Leu Asn Lys Leu Lys Gln Asp Asn Leu Leu Gln Lys Lys Gly
 130 135 140
 Phe Pro Val Ser Tyr Asp Thr Pro Lys Leu Ile Arg Phe Leu Ala Asp
 145 150 155 160
 Val Lys Ser Gly Lys Ser Asn Val Thr Ala Pro Ile Tyr Ser His Leu
 165 170 175
 Thr Tyr Asp Ile Ile Pro Asp Lys Phe Asp Val Val Asp Lys Pro Asp
 180 185 190
 Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr Gly Asn Asn Lys
 195 200 205
 Thr Asp Gln Thr Phe Val Ser Asp Phe Val Asp Phe Ser Ile Tyr Val
 210 215 220
 Asp Ala Glu Glu Lys Leu Leu Lys Glu Trp Tyr Ile Lys Arg Phe Leu
 225 230 235 240
 Lys Phe Arg Glu Ser Ala Phe Asn Asp Pro Asn Ser Tyr Phe Lys His
 245 250 255
 Tyr Ala Ser Leu Ser Lys Glu Glu Ala Ile Ala Thr Ala Ser Lys Ile
 260 265 270
 Trp Asp Glu Ile Asn Gly Leu Asn Leu Asn Gln Asn Ile Leu Pro Thr
 275 280 285
 Arg Glu Arg Ala Asn Leu Ile Leu Lys Lys Gly His Asn His Gln Val
 290 295 300
 Glu Leu Ile Lys Leu Arg Lys
 305 310

<210> 2
 <211> 316
 <212> PRT
 <213> Escherichia coli

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 Met Ser Ile Lys Glu Gln Thr Leu Met Thr Pro Tyr Leu Gln Phe Asp
 1 5 10 15
 Arg Asn Gln Trp Ala Ala Leu Arg Asp Ser Val Pro Met Thr Leu Ser
 20 25 30
 Glu Asp Glu Ile Ala Arg Leu Lys Gly Ile Asn Glu Asp Leu Ser Leu
 35 40 45
 Glu Glu Val Ala Glu Ile Tyr Leu Pro Leu Ser Arg Leu Leu Asn Phe
 50 55 60
 Tyr Ile Ser Ser Asn Leu Arg Arg Gln Ala Val Leu Glu Gln Phe Leu
 65 70 75 80

- 3 -

Gly Thr Asn Gly Gln Arg Ile Pro Tyr Ile Ile Ser Ile Ala Gly Ser
 85 90 95
 Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala Leu Leu
 100 105 110
 Ser Arg Trp Pro Glu His Arg Arg Val Glu Leu Ile Thr Thr Asp Gly
 115 120 125
 Phe Leu His Pro Asn Gln Val Leu Lys Glu Arg Gly Leu Met Lys Lys
 130 135 140
 Lys Gly Phe Pro Glu Ser Tyr Asp Met His Arg Leu Val Lys Phe Val
 145 150 155 160
 Ser Asp Leu Lys Ser Gly Val Pro Asn Val Thr Ala Pro Val Tyr Ser
 165 170 175
 His Leu Ile Tyr Asp Val Ile Pro Asp Gly Asp Lys Thr Val Val Gln
 180 185 190
 Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Ser Gly Met
 195 200 205
 Asp Tyr Pro His Asp Pro His His Val Phe Val Ser Asp Phe Val Asp
 210 215 220
 Phe Ser Ile Tyr Val Asp Ala Pro Glu Asp Leu Leu Gln Thr Trp Tyr
 225 230 235 240
 Ile Asn Arg Phe Leu Lys Phe Arg Glu Gly Ala Phe Thr Asp Pro Asp
 245 250 255
 Ser Tyr Phe His Asn Tyr Ala Lys Leu Thr Lys Glu Glu Ala Ile Lys
 260 265 270
 Thr Ala Met Thr Leu Trp Lys Glu Ile Asn Trp Leu Asn Leu Lys Gln
 275 280 285
 Asn Ile Leu Pro Thr Arg Glu Arg Ala Ser Leu Ile Leu Thr Lys Ser
 290 295 300
 Ala Asn His Ala Val Glu Glu Val Arg Leu Arg Lys
 305 310 315

<210> 3

<211> 319

<212> PRT

<213> Bacillus subtilis

<400> 3

Met Lys Asn Lys Glu Leu Asn Leu His Thr Leu Tyr Thr Gln His Asn
 1 5 10 15

Arg Glu Ser Trp Ser Gly Phe Gly Gly His Leu Ser Ile Ala Val Ser
 20 25 30

- 4 -

Glu Glu Glu Ala Lys Ala Val Glu Gly Leu Asn Asp Tyr Leu Ser Val
 35 40 45
 Glu Glu Val Glu Thr Ile Tyr Ile Pro Leu Val Arg Leu Leu His Leu
 50 55 60
 His Val Lys Ser Ala Ala Glu Arg Asn Lys His Val Asn Val Phe Leu
 65 70 75 80
 Lys His Pro His Ser Ala Lys Ile Pro Phe Ile Ile Gly Ile Ala Gly
 85 90 95
 Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Ile Leu Gln Lys Leu
 100 105 110
 Leu Ser Arg Leu Pro Asp Arg Pro Lys Val Ser Leu Ile Thr Thr Asp
 115 120 125
 Gly Phe Leu Phe Pro Thr Ala Glu Leu Lys Lys Lys Asn Met Met Ser
 130 135 140
 Arg Lys Gly Phe Pro Glu Ser Tyr Asp Val Lys Ala Leu Leu Glu Phe
 145 150 155 160
 Leu Asn Asp Leu Lys Ser Gly Lys Asp Ser Val Lys Ala Pro Val Tyr
 165 170 175
 Ser His Leu Thr Tyr Asp Arg Glu Glu Gly Val Phe Glu Val Val Glu
 180 185 190
 Gln Ala Asp Ile Val Ile Ile Glu Gly Ile Asn Val Leu Gln Ser Pro
 195 200 205
 Thr Leu Glu Asp Asp Arg Glu Asn Pro Arg Ile Phe Val Ser Asp Phe
 210 215 220
 Phe Asp Phe Ser Ile Tyr Val Asp Ala Glu Glu Ser Arg Ile Phe Thr
 225 230 235 240
 Trp Tyr Leu Glu Arg Phe Arg Leu Leu Arg Glu Thr Ala Phe Gln Asn
 245 250 255
 Pro Asp Ser Tyr Phe His Lys Phe Lys Asp Leu Ser Asp Gln Glu Ala
 260 265 270
 Asp Glu Met Ala Ala Ser Ile Trp Glu Ser Val Asn Arg Pro Asn Leu
 275 280 285
 Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg Ser Asp Leu Ile Leu Arg
 290 295 300
 Lys Gly Asp Gly His Lys Val Glu Glu Val Leu Val Arg Arg Val
 305 310 315

<210> 4
 <211> 312
 <212> PRT

- 5 -

<213> Mycobacterium leprae

<400> 4

Met	Pro	Arg	Leu	Ser	Glu	Pro	Ser	Pro	Tyr	Val	Glu	Phe	Asp	Arg	Lys	1	5	10	15
Gln	Trp	Arg	Ala	Leu	Arg	Met	Ser	Thr	Pro	Leu	Ala	Leu	Thr	Glu	Glu	20	25	30	
Glu	Leu	Ile	Gly	Leu	Arg	Gly	Leu	Gly	Glu	Gln	Ile	Asp	Leu	Leu	Glu	35	40	45	
Val	Glu	Glu	Val	Tyr	Leu	Pro	Leu	Ala	Arg	Leu	Ile	His	Leu	Gln	Val	50	55	60	
Ala	Ala	Arg	Gln	Arg	Leu	Phe	Ala	Ala	Thr	Ala	Glu	Phe	Leu	Gly	Glu	65	70	75	80
Pro	Gln	Gln	Asn	Pro	Gly	Arg	Pro	Val	Pro	Phe	Ile	Ile	Gly	Val	Ala	85	90	95	
Gly	Ser	Val	Ala	Val	Gly	Lys	Ser	Thr	Thr	Ala	Arg	Val	Leu	Gln	Ala	100	105	110	
Leu	Leu	Ala	Arg	Trp	Asp	His	His	Thr	Arg	Val	Asp	Leu	Val	Thr	Thr	115	120	125	
Asp	Gly	Phe	Leu	Tyr	Pro	Asn	Ala	Glu	Leu	Gly	Arg	Arg	Asn	Leu	Met	130	135	140	
His	Arg	Lys	Gly	Phe	Pro	Glu	Ser	Tyr	Asn	Arg	Arg	Ala	Leu	Met	Arg	145	150	155	160
Phe	Val	Thr	Ser	Val	Lys	Ser	Gly	Ala	Asp	Tyr	Ala	Cys	Ala	Pro	Val	165	170	175	
Tyr	Ser	His	Leu	Arg	Tyr	Asp	Thr	Ile	Pro	Gly	Ala	Lys	His	Val	Val	180	185	190	
Arg	His	Pro	Asp	Ile	Leu	Ile	Leu	Glu	Gly	Leu	Asn	Val	Leu	Gln	Thr	195	200	205	
Gly	Pro	Thr	Leu	Met	Val	Ser	Asp	Leu	Phe	Asp	Phe	Ser	Leu	Tyr	Val	210	215	220	
Asp	Ala	Arg	Ile	Gln	Asp	Ile	Glu	Gln	Trp	Tyr	Val	Ser	Arg	Phe	Leu	225	230	235	240
Ala	Met	Arg	Gly	Thr	Ala	Phe	Ala	Asp	Pro	Glu	Ser	His	Phe	His	His	245	250	255	
Tyr	Ser	Ala	Leu	Thr	Asp	Ser	Lys	Ala	Ile	Ile	Ala	Ala	Arg	Glu	Ile	260	265	270	
Trp	Arg	Ser	Ile	Asn	Arg	Pro	Asn	Leu	Val	Glu	Asn	Ile	Leu	Pro	Thr	275	280	285	
Arg	Pro	Arg	Ala	Thr	Leu	Val	Leu	Arg	Lys	Asp	Ala	Asp	His	Ser	Ile				

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290 295 300
 Asn Arg Leu Arg Leu Arg Lys Leu
 305 310

<210> 5
 <211> 312
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 5
 Met Ser Arg Leu Ser Glu Pro Ser Pro Tyr Val Glu Phe Asp Arg Arg
 1 5 10 15

Gln Trp Arg Ala Leu Arg Met Ser Thr Pro Leu Ala Leu Thr Glu Glu
 20 25 30

Glu Leu Val Gly Leu Arg Gly Leu Gly Glu Gln Ile Asp Leu Leu Glu
 35 40 45

Val Glu Glu Val Tyr Leu Pro Leu Ala Arg Leu Ile His Leu Gln Val
 50 55 60

Ala Ala Arg Gln Arg Leu Phe Ala Ala Thr Ala Glu Phe Leu Gly Glu
 65 70 75 80

Pro Gln Gln Asn Pro Asp Arg Pro Val Pro Phe Ile Ile Gly Val Ala
 85 90 95

Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala
 100 105 110

Leu Leu Ala Arg Trp Asp His His Pro Arg Val Asp Leu Val Thr Thr
 115 120 125

Asp Gly Phe Leu Tyr Pro Asn Ala Glu Leu Gln Arg Arg Asn Leu Met
 130 135 140

His Arg Lys Gly Phe Pro Glu Ser Tyr Asn Arg Arg Ala Leu Met Arg
 145 150 155 160

Phe Val Thr Ser Val Lys Ser Gly Ser Asp Tyr Ala Cys Ala Pro Val
 165 170 175

Tyr Ser His Leu His Tyr Asp Ile Ile Pro Gly Ala Glu Gln Val Val
 180 185 190

Arg His Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr
 195 200 205

Gly Pro Thr Leu Met Val Ser Asp Leu Phe Asp Phe Ser Leu Tyr Val
 210 215 220

Asp Ala Arg Ile Glu Asp Ile Glu Gln Trp Tyr Val Ser Arg Phe Leu
 225 230 235 240

Ala Met Arg Thr Thr Ala Phe Ala Asp Pro Glu Ser His Phe His His

- 7 -

				245						250						255
Tyr	Ala	Ala	Phe	Ser	Asp	Ser	Gln	Ala	Val	Val	Ala	Ala	Arg	Glu	Ile	
			260					265					270			
Trp	Arg	Thr	Ile	Asn	Arg	Pro	Asn	Leu	Val	Glu	Asn	Ile	Leu	Pro	Thr	
		275					280					285				
Arg	Pro	Arg	Ala	Thr	Leu	Val	Leu	Arg	Lys	Asp	Ala	Asp	His	Ser	Ile	
	290					295					300					
Asn	Arg	Leu	Arg	Leu	Arg	Lys	Leu									
305					310											

<210> 6

<211> 329

<212> PRT

<213> Streptomyces coelicolor

<400> 6

Met	Ile	Ser	Pro	Val	Pro	Ser	Ile	Pro	Arg	Ser	Ala	His	Arg	Gln	Arg
1				5					10					15	
Pro	Glu	Ala	Thr	Pro	Tyr	Val	Asp	Leu	Thr	Arg	Pro	Glu	Trp	Ser	Ala
			20					25					30		
Leu	Arg	Asp	Lys	Thr	Pro	Leu	Pro	Leu	Thr	Ala	Glu	Glu	Val	Glu	Lys
		35					40					45			
Leu	Arg	Gly	Leu	Gly	Asp	Val	Ile	Asp	Leu	Asp	Glu	Val	Arg	Asp	Ile
	50					55					60				
Tyr	Leu	Pro	Leu	Ser	Arg	Leu	Leu	Asn	Leu	Tyr	Val	Gly	Ala	Thr	Asp
65					70					75					80
Gly	Leu	Arg	Gly	Ala	Leu	Asn	Thr	Phe	Leu	Gly	Glu	Gln	Gly	Ser	Gln
				85					90					95	
Ser	Gly	Thr	Pro	Phe	Val	Ile	Gly	Val	Ala	Gly	Ser	Val	Ala	Val	Gly
			100					105					110		
Lys	Ser	Thr	Val	Ala	Arg	Leu	Leu	Gln	Ala	Leu	Leu	Ser	Arg	Trp	Pro
		115					120					125			
Glu	His	Pro	Arg	Val	Glu	Leu	Val	Thr	Thr	Asp	Gly	Phe	Leu	Leu	Pro
	130					135					140				
Thr	Arg	Glu	Leu	Glu	Ala	Arg	Gly	Leu	Met	Ser	Arg	Lys	Gly	Phe	Pro
145					150					155					160
Glu	Ser	Tyr	Asp	Arg	Arg	Ala	Leu	Thr	Arg	Phe	Val	Ala	Asp	Ile	Lys
				165					170					175	
Ala	Gly	Lys	Ala	Glu	Val	Thr	Ala	Pro	Val	Tyr	Ser	His	Leu	Ile	Tyr
			180					185					190		
Asp	Ile	Val	Pro	Asp	Gln	Arg	Leu	Val	Val	Arg	Arg	Pro	Asp	Ile	Leu

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	195		200		205										
Ile	Val	Glu	Gly	Leu	Asn	Val	Leu	Gln	Pro	Ala	Leu	Pro	Gly	Lys	Asp
	210					215					220				
Gly	Arg	Thr	Arg	Val	Gly	Leu	Ala	Asp	Tyr	Phe	Asp	Phe	Ser	Val	Tyr
225					230					235					240
Val	Asp	Ala	Arg	Thr	Glu	Asp	Ile	Glu	Arg	Trp	Tyr	Leu	Asn	Arg	Phe
				245					250					255	
Arg	Lys	Leu	Arg	Ala	Thr	Ala	Phe	Gln	Asn	Pro	Ser	Ser	Tyr	Phe	Arg
			260					265					270		
Lys	Tyr	Thr	Gln	Val	Ser	Glu	Glu	Glu	Ala	Leu	Asp	Tyr	Ala	Arg	Thr
		275					280					285			
Thr	Trp	Arg	Thr	Ile	Asn	Lys	Pro	Asn	Leu	Val	Glu	Asn	Val	Ala	Pro
	290					295					300				
Thr	Arg	Gly	Arg	Ala	Thr	Leu	Val	Leu	Arg	Lys	Gly	Pro	Asp	His	Lys
305					310					315					320
Val	Gln	Arg	Leu	Ser	Leu	Arg	Lys	Leu							
				325											

<210> 7

<211> 265

<212> PRT

<213> Streptomyces coelicolor

<400> 7

Met	Leu	Leu	Thr	Ile	Asp	Val	Gly	Asn	Thr	His	Thr	Val	Leu	Gly	Leu
1				5					10					15	
Phe	Asp	Gly	Glu	Asp	Ile	Val	Glu	His	Trp	Arg	Ile	Ser	Thr	Asp	Ser
			20					25					30		
Arg	Arg	Thr	Ala	Asp	Glu	Leu	Ala	Val	Leu	Leu	Gln	Gly	Leu	Met	Gly
		35					40					45			
Met	His	Pro	Leu	Leu	Gly	Asp	Glu	Leu	Gly	Asp	Gly	Ile	Asp	Gly	Ile
	50					55					60				
Ala	Ile	Cys	Ala	Thr	Val	Pro	Ser	Val	Leu	His	Glu	Leu	Arg	Glu	Val
65					70					75					80
Thr	Arg	Arg	Tyr	Tyr	Gly	Asp	Val	Pro	Ala	Val	Leu	Val	Glu	Pro	Gly
			85						90					95	
Val	Lys	Thr	Gly	Val	Pro	Ile	Leu	Thr	Asp	His	Pro	Lys	Glu	Val	Gly
			100					105					110		
Ala	Asp	Arg	Ile	Ile	Asn	Ala	Val	Ala	Ala	Val	Glu	Leu	Tyr	Gly	Gly
	115						120					125			
Pro	Ala	Ile	Val	Val	Asp	Phe	Gly	Thr	Ala	Thr	Thr	Phe	Asp	Ala	Val

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130 135 140
 Ser Ala Arg Gly Glu Tyr Ile Gly Gly Val Ile Ala Pro Gly Ile Glu
 145 150 155 160
 Ile Ser Val Glu Ala Leu Gly Val Lys Gly Ala Gln Leu Arg Lys Ile
 165 170 175
 Glu Val Ala Arg Pro Arg Ser Val Ile Gly Lys Asn Thr Val Glu Ala
 180 185 190
 Met Gln Ser Gly Ile Val Tyr Gly Phe Ala Gly Gln Val Asp Gly Val
 195 200 205
 Val Asn Arg Met Ala Arg Glu Leu Ala Asp Asp Pro Asp Asp Val Thr
 210 215 220
 Val Ile Ala Thr Gly Gly Leu Ala Pro Met Val Leu Gly Glu Ser Ser
 225 230 235 240
 Val Ile Asp Glu His Glu Pro Trp Leu Thr Leu Met Gly Leu Arg Leu
 245 250 255
 Val Tyr Glu Arg Asn Val Ser Arg Met
 260 265

<210> 8

<211> 272

<212> PRT

<213> Mycobacterium tuberculosis

<400> 8

Met Leu Leu Ala Ile Asp Val Arg Asn Thr His Thr Val Val Gly Leu
 1 5 10 15
 Leu Ser Gly Met Lys Glu His Ala Lys Val Val Gln Gln Trp Arg Ile
 20 25 30
 Arg Thr Glu Ser Glu Val Thr Ala Asp Glu Leu Ala Leu Thr Ile Asp
 35 40 45
 Gly Leu Ile Gly Glu Asp Ser Glu Arg Leu Thr Gly Thr Ala Ala Leu
 50 55 60
 Ser Thr Val Pro Ser Val Leu His Glu Val Arg Ile Met Leu Asp Gln
 65 70 75 80
 Tyr Trp Pro Ser Val Pro His Val Leu Ile Glu Pro Gly Val Arg Thr
 85 90 95
 Gly Ile Pro Leu Leu Val Asp Asn Pro Lys Glu Val Gly Ala Asp Arg
 100 105 110
 Ile Val Asn Cys Leu Ala Ala Tyr Asp Arg Phe Arg Lys Ala Ala Ile
 115 120 125
 Val Val Asp Phe Gly Ser Ser Ile Cys Val Asp Val Val Ser Ala Lys

- 10 -

130						135						140				
Gly	Glu	Phe	Leu	Gly	Gly	Ala	Ile	Ala	Pro	Gly	Val	Gln	Val	Ser	Ser	
145					150					155					160	
Asp	Ala	Ala	Ala	Ala	Arg	Ser	Ala	Ala	Leu	Arg	Arg	Val	Glu	Leu	Ala	
				165					170					175		
Arg	Pro	Arg	Ser	Val	Val	Gly	Lys	Asn	Thr	Val	Glu	Cys	Met	Gln	Ala	
			180					185					190			
Gly	Ala	Val	Phe	Gly	Phe	Ala	Gly	Leu	Val	Asp	Gly	Leu	Val	Gly	Arg	
		195					200					205				
Ile	Arg	Glu	Asp	Val	Ser	Gly	Phe	Ser	Val	Asp	His	Asp	Val	Ala	Ile	
210						215				220						
Val	Ala	Thr	Gly	His	Thr	Ala	Pro	Leu	Leu	Leu	Pro	Glu	Leu	His	Thr	
225					230					235					240	
Val	Asp	His	Tyr	Asp	Gln	His	Leu	Thr	Leu	Gln	Gly	Leu	Arg	Leu	Val	
				245				250						255		
Phe	Glu	Arg	Asn	Leu	Glu	Val	Gln	Arg	Gly	Arg	Leu	Lys	Thr	Ala	Arg	
			260					265					270			

<210> 9

<211> 258

<212> PRT

<213> Bacillus subtilis

<400> 9

Leu	Leu	Leu	Val	Ile	Asp	Val	Gly	Asn	Thr	Asn	Thr	Val	Leu	Gly	Val	
1				5				10					15			
Tyr	His	Asp	Gly	Lys	Leu	Glu	Tyr	His	Trp	Arg	Ile	Glu	Thr	Ser	Arg	
			20					25					30			
His	Lys	Thr	Glu	Asp	Glu	Phe	Gly	Met	Ile	Leu	Arg	Ser	Leu	Phe	Asp	
			35				40					45				
His	Ser	Gly	Leu	Met	Phe	Glu	Gln	Ile	Asp	Gly	Ile	Ile	Ile	Ser	Ser	
	50					55					60					
Val	Val	Pro	Pro	Ile	Met	Phe	Ala	Leu	Glu	Arg	Met	Cys	Thr	Lys	Tyr	
65					70					75					80	
Phe	His	Ile	Glu	Pro	Gln	Ile	Val	Gly	Pro	Gly	Met	Lys	Thr	Gly	Leu	
				85				90						95		
Asn	Ile	Lys	Tyr	Asp	Asn	Pro	Lys	Glu	Val	Gly	Ala	Asp	Arg	Ile	Val	
			100					105					110			
Asn	Ala	Val	Ala	Ala	Ile	His	Leu	Tyr	Gly	Asn	Pro	Leu	Ile	Val	Val	
			115				120					125				

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Asp	Phe	Gly	Thr	Ala	Thr	Thr	Tyr	Cys	Tyr	Ile	Asp	Glu	Asn	Lys	Gln
130						135					140				
Tyr	Met	Gly	Gly	Ala	Ile	Ala	Pro	Gly	Ile	Thr	Ile	Ser	Thr	Glu	Ala
145					150					155					160
Leu	Tyr	Ser	Arg	Ala	Ala	Lys	Leu	Pro	Arg	Ile	Glu	Ile	Thr	Arg	Pro
				165					170					175	
Asp	Asn	Ile	Ile	Gly	Lys	Asn	Thr	Val	Ser	Ala	Met	Gln	Ser	Gly	Ile
			180					185					190		
Leu	Phe	Gly	Tyr	Val	Gly	Gln	Val	Glu	Gly	Ile	Val	Lys	Arg	Met	Lys
		195					200					205			
Trp	Gln	Ala	Lys	Gln	Asp	Leu	Lys	Val	Ile	Ala	Thr	Gly	Gly	Leu	Ala
210						215					220				
Pro	Leu	Ile	Ala	Asn	Glu	Ser	Asp	Cys	Ile	Asp	Ile	Val	Asp	Pro	Phe
225					230					235					240
Leu	Thr	Leu	Lys	Gly	Leu	Glu	Leu	Ile	Tyr	Glu	Arg	Asn	Arg	Val	Gly
				245					250					255	

Ser Val

<210> 10

<211> 262

<212> PRT

<213> Deinococcus radiopugnans

<400> 10

Met	Pro	Ala	Phe	Pro	Leu	Leu	Ala	Val	Asp	Ile	Gly	Asn	Thr	Thr	Thr
1				5					10					15	
Val	Leu	Gly	Leu	Ala	Asp	Ala	Ser	Gly	Ala	Leu	Thr	His	Thr	Trp	Arg
			20					25					30		
Ile	Arg	Thr	Asn	Arg	Glu	Met	Leu	Pro	Asp	Asp	Leu	Ala	Leu	Gln	Leu
		35					40					45			
His	Gly	Leu	Phe	Thr	Leu	Ala	Gly	Ala	Pro	Ile	Pro	Arg	Ala	Ala	Val
	50					55					60				
Leu	Ser	Ser	Val	Ala	Pro	Pro	Val	Gly	Glu	Asn	Tyr	Ala	Leu	Ala	Leu
65					70					75					80
Lys	Arg	His	Phe	Met	Ile	Asp	Ala	Phe	Ala	Val	Ser	Ala	Glu	Asn	Leu
				85					90					95	
Pro	Asp	Val	Thr	Val	Glu	Leu	Asp	Thr	Pro	Gly	Ser	Val	Gly	Ala	Asp
			100					105					110		
Arg	Leu	Cys	Asn	Leu	Phe	Gly	Ala	Glu	Lys	Tyr	Leu	Gly	Gly	Leu	Asp

- 12 -

	115		120		125
Tyr	Ala Val Val Val Asp Phe	Gly Thr Ser Thr Asn Phe Asp Val Val			
130		135		140	
Gly Arg Gly Arg Arg Phe Leu	Gly Gly Ile Leu Ala Thr Gly Ala Gln				
145	150		155		160
Val Ser Ala Asp Ala Leu Phe	Ala Arg Ala Ala Lys Leu Pro Arg Ile				
	165		170		175
Thr Leu Gln Ala Pro Glu Thr	Ala Ile Gly Lys Asn Thr Val His Ala				
	180		185		190
Leu Gln Ser Gly Leu Val Phe	Gly Tyr Ala Glu Met Val Asp Gly Leu				
	195		200		205
Leu Arg Arg Ile Arg Ala Glu	Leu Pro Gly Glu Ala Val Ala Val Ala				
	210		215		220
Thr Gly Gly Phe Ser Arg Thr	Val Gln Gly Ile Cys Gln Glu Ile Asp				
225	230		235		240
Tyr Tyr Asp Glu Thr Leu Thr	Leu Arg Gly Leu Val Glu Leu Trp Ala				
	245		250		255
Ser Arg Ser Glu Val Arg					
	260				

<210> 11
 <211> 212
 <212> PRT
 <213> Desulfovibrio vulgaris

<400> 11
 Met Thr Gln His Phe Leu Leu Phe Asp Ile Gly Asn Thr Asn Val Lys
 1 5 10 15
 Ile Gly Ile Ala Val Glu Thr Ala Val Leu Thr Ser Tyr Val Leu Pro
 20 25 30
 Thr Asp Pro Gly Gln Thr Thr Asp Ser Ile Gly Leu Arg Leu Leu Glu
 35 40 45
 Val Leu Arg His Ala Gly Leu Gly Pro Ala Asp Val Gly Ala Cys Val
 50 55 60
 Ala Ser Ser Val Val Pro Gly Val Asn Pro Leu Ile Arg Arg Ala Cys
 65 70 75 80
 Glu Arg Tyr Leu Tyr Arg Lys Leu Leu Phe Ala Pro Gly Asp Ile Ala
 85 90 95
 Ile Pro Leu Asp Asn Arg Tyr Glu Arg Pro Ala Glu Val Gly Ala Asp
 100 105 110
 Arg Leu Val Ala Ala Tyr Ala Ala Arg Arg Leu Tyr Pro Gly Pro Arg

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	115		120		125											
Ser	Leu	Val	Ser	Val	Asp	Phe	Gly	Thr	Ala	Thr	Thr	Phe	Asp	Cys	Val	
	130					135					140					
Glu	Gly	Gly	Ala	Tyr	Leu	Gly	Gly	Leu	Ile	Cys	Pro	Gly	Val	Leu	Ser	
145					150					155					160	
Ser	Ala	Gly	Ala	Leu	Ser	Ser	Arg	Thr	Ala	Lys	Leu	Pro	Arg	Ile	Ser	
				165					170					175		
Leu	Glu	Val	Glu	Glu	Asp	Ser	Pro	Val	Ile	Gly	Arg	Ser	Thr	Thr	Thr	
			180					185					190			
Ser	Leu	Asn	His	Gly	Phe	Ile	Phe	Gly	Phe	Ala	Ala	Met	Thr	Glu	Gly	
		195					200					205				
Val	Leu	Ala	Ala													
	210															

<210> 12

<211> 246

<212> PRT

<213> Thermotoga maritima

<400> 12

Met	Tyr	Leu	Leu	Val	Asp	Val	Gly	Asn	Thr	His	Ser	Val	Phe	Ser	Ile	
1				5					10					15		
Thr	Glu	Asp	Gly	Lys	Thr	Phe	Arg	Arg	Trp	Arg	Leu	Ser	Thr	Gly	Val	
			20					25					30			
Phe	Gln	Thr	Glu	Asp	Glu	Leu	Phe	Ser	His	Leu	His	Pro	Leu	Leu	Gly	
		35					40					45				
Asp	Ala	Met	Arg	Glu	Ile	Lys	Gly	Ile	Gly	Val	Ala	Ser	Val	Val	Pro	
	50					55					60					
Thr	Gln	Asn	Thr	Val	Ile	Glu	Arg	Phe	Ser	Gln	Lys	Tyr	Phe	His	Ile	
65					70					75					80	
Ser	Pro	Ile	Trp	Val	Lys	Ala	Lys	Asn	Gly	Cys	Val	Lys	Trp	Asn	Val	
				85					90					95		
Lys	Asn	Pro	Ser	Glu	Val	Gly	Ala	Asp	Arg	Val	Ala	Asn	Val	Val	Ala	
			100					105					110			
Phe	Val	Lys	Glu	Tyr	Gly	Lys	Asn	Gly	Ile	Ile	Ile	Asp	Met	Gly	Thr	
		115					120					125				
Ala	Thr	Thr	Val	Asp	Leu	Val	Val	Asn	Gly	Ser	Tyr	Glu	Gly	Gly	Ala	
	130					135					140					
Ile	Leu	Pro	Gly	Phe	Phe	Met	Met	Val	His	Ser	Leu	Phe	Arg	Gly	Thr	
145					150					155					160	
Ala	Lys	Leu	Pro	Leu	Val	Glu	Val	Lys	Pro	Ala	Asp	Phe	Val	Val	Gly	

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				165					170					175			
Lys	Asp	Thr	Glu	Glu	Asn	Ile	Arg	Leu	Gly	Val	Val	Asn	Gly	Ser	Val		
			180					185					190				
Tyr	Ala	Leu	Glu	Gly	Ile	Ile	Gly	Arg	Ile	Lys	Glu	Val	Tyr	Gly	Asp		
		195					200					205					
Leu	Pro	Val	Val	Leu	Thr	Gly	Gly	Gln	Ser	Lys	Ile	Val	Lys	Asp	Met		
	210					215					220						
Ile	Lys	His	Glu	Ile	Phe	Asp	Glu	Asp	Leu	Thr	Ile	Lys	Gly	Val	Tyr		
225					230					235					240		
His	Phe	Cys	Phe	Gly	Asp												
				245													

<210> 13

<211> 273

<212> PRT

<213> Treponema pallidum

<400> 13

Met	Leu	Leu	Ile	Asp	Val	Gly	Asn	Ser	His	Val	Val	Phe	Gly	Ile	Gln		
1				5					10					15			
Gly	Glu	Asn	Gly	Gly	Arg	Val	Cys	Val	Arg	Glu	Leu	Phe	Arg	Leu	Ala		
			20					25					30				
Pro	Asp	Ala	Arg	Lys	Thr	Gln	Asp	Glu	Tyr	Ser	Leu	Leu	Ile	His	Ala		
		35					40					45					
Leu	Cys	Glu	Arg	Ala	Gly	Val	Gly	Arg	Ala	Ser	Leu	Arg	Asp	Ala	Phe		
	50					55					60						
Ile	Ser	Ser	Val	Val	Pro	Val	Leu	Thr	Lys	Thr	Ile	Ala	Asp	Ala	Val		
65					70					75					80		
Ala	Gln	Ile	Ser	Gly	Val	Gln	Pro	Val	Val	Phe	Gly	Pro	Trp	Ala	Tyr		
				85					90					95			
Glu	His	Leu	Pro	Val	Arg	Ile	Pro	Glu	Pro	Val	Arg	Ala	Glu	Ile	Gly		
			100					105					110				
Thr	Asp	Leu	Val	Ala	Asn	Ala	Val	Ala	Ala	Tyr	Val	His	Phe	Arg	Ser		
		115					120					125					
Ala	Cys	Val	Val	Val	Asp	Cys	Gly	Thr	Ala	Leu	Thr	Phe	Thr	Ala	Val		
	130					135					140						
Asp	Gly	Thr	Gly	Leu	Ile	Gln	Gly	Val	Ala	Ile	Ala	Pro	Gly	Leu	Arg		
145					150					155					160		
Thr	Ala	Val	Gln	Ser	Leu	His	Thr	Gly	Thr	Ala	Gln	Leu	Pro	Leu	Val		
				165					170					175			
Pro	Leu	Ala	Leu	Pro	Asp	Ser	Val	Leu	Gly	Lys	Asp	Thr	Thr	His	Ala		

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			180						185				190			
Val	Gln	Ala	Gly	Val	Val	Arg	Gly	Thr	Leu	Phe	Val	Ile	Arg	Ala	Met	
		195					200					205				
Ile	Ala	Gln	Cys	Gln	Lys	Glu	Leu	Gly	Cys	Arg	Cys	Ala	Ala	Val	Ile	
	210					215					220					
Thr	Gly	Gly	Leu	Ser	Arg	Leu	Phe	Ser	Ser	Glu	Val	Asp	Phe	Pro	Pro	
225					230					235					240	
Ile	Asp	Ala	Gln	Leu	Thr	Leu	Ser	Gly	Leu	Ala	His	Ile	Ala	Arg	Leu	
				245					250					255		
Val	Pro	Thr	Ser	Leu	Leu	Pro	Pro	Ala	Thr	Val	Ser	Gly	Ser	Ser	Gly	
			260					265					270			

Asn

<210> 14
 <211> 262
 <212> PRT
 <213> *Borrelia burgdorferi*

<400> 14

Met	Asn	Lys	Pro	Leu	Leu	Ser	Glu	Leu	Ile	Ile	Asp	Ile	Gly	Asn	Thr
1				5					10					15	
Ser	Ile	Ala	Phe	Ala	Leu	Phe	Lys	Asp	Asn	Gln	Val	Asn	Leu	Phe	Ile
			20					25					30		
Lys	Met	Lys	Thr	Asn	Leu	Met	Leu	Arg	Tyr	Asp	Glu	Val	Tyr	Ser	Phe
		35					40					45			
Phe	Glu	Glu	Asn	Phe	Asp	Phe	Asn	Val	Asn	Lys	Val	Phe	Ile	Ser	Ser
	50					55					60				
Val	Val	Pro	Ile	Leu	Asn	Glu	Thr	Phe	Lys	Asn	Val	Ile	Phe	Ser	Phe
65					70					75					80
Phe	Lys	Ile	Lys	Pro	Leu	Phe	Ile	Gly	Phe	Asp	Leu	Asn	Tyr	Asp	Leu
				85				90						95	
Thr	Phe	Asn	Pro	Tyr	Lys	Ser	Asp	Lys	Phe	Leu	Leu	Gly	Ser	Asp	Val
			100					105					110		
Phe	Ala	Asn	Leu	Val	Ala	Ala	Ile	Glu	Asn	Tyr	Ser	Phe	Glu	Asn	Val
		115					120					125			
Leu	Val	Val	Asp	Leu	Gly	Thr	Ala	Cys	Thr	Ile	Phe	Ala	Val	Ser	Arg
	130					135						140			
Gln	Asp	Gly	Ile	Leu	Gly	Gly	Ile	Ile	Asn	Ser	Gly	Pro	Leu	Ile	Asn
145					150				155						160
Phe	Asn	Ser	Leu	Leu	Asp	Asn	Ala	Tyr	Leu	Ile	Lys	Lys	Phe	Pro	Ile

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				165					170					175			
Ser	Thr	Pro	Asn	Asn	Leu	Leu	Glu	Arg	Thr	Thr	Ser	Gly	Ser	Val	Asn		
			180					185					190				
Ser	Gly	Leu	Phe	Tyr	Gln	Tyr	Lys	Tyr	Leu	Ile	Glu	Gly	Val	Tyr	Arg		
		195					200					205					
Asp	Ile	Lys	Gln	Met	Tyr	Lys	Lys	Lys	Phe	Asn	Leu	Ile	Ile	Thr	Gly		
	210					215					220						
Gly	Asn	Ala	Asp	Leu	Ile	Leu	Ser	Leu	Ile	Glu	Ile	Glu	Phe	Ile	Phe		
225					230					235					240		
Asn	Ile	His	Leu	Thr	Val	Glu	Gly	Val	Arg	Ile	Leu	Gly	Asn	Ser	Ile		
				245					250					255			
Asp	Phe	Lys	Phe	Val	Asn												
			260														

<210> 15
 <211> 229
 <212> PRT
 <213> Aquifex aeolicus

<400> 15																	
Met	Arg	Phe	Leu	Thr	Val	Asp	Val	Gly	Asn	Ser	Ser	Val	Asp	Ile	Ala		
1				5					10					15			
Leu	Trp	Glu	Gly	Lys	Lys	Val	Lys	Asp	Phe	Leu	Lys	Leu	Ser	His	Glu		
			20					25					30				
Glu	Phe	Leu	Lys	Glu	Glu	Phe	Pro	Lys	Leu	Lys	Ala	Leu	Gly	Ile	Ser		
		35					40					45					
Val	Lys	Gln	Ser	Phe	Ser	Glu	Lys	Val	Arg	Gly	Lys	Ile	Pro	Lys	Ile		
	50					55					60						
Lys	Phe	Leu	Lys	Lys	Glu	Asn	Phe	Pro	Ile	Gln	Val	Asp	Tyr	Lys	Thr		
65				70						75					80		
Pro	Glu	Thr	Leu	Gly	Thr	Asp	Arg	Val	Ala	Leu	Ala	Tyr	Ser	Ala	Lys		
				85					90					95			
Lys	Phe	Tyr	Gly	Lys	Asn	Val	Val	Val	Ile	Ser	Ala	Gly	Thr	Ala	Leu		
			100					105					110				
Val	Ile	Asp	Leu	Val	Leu	Glu	Gly	Lys	Phe	Lys	Gly	Gly	Phe	Ile	Thr		
		115					120					125					
Leu	Gly	Leu	Gly	Lys	Lys	Leu	Lys	Ile	Leu	Ser	Asp	Leu	Ala	Glu	Gly		
	130					135					140						
Ile	Pro	Glu	Phe	Phe	Pro	Glu	Glu	Val	Glu	Ile	Phe	Leu	Gly	Arg	Ser		
145					150					155					160		
Thr	Arg	Glu	Cys	Val	Leu	Gly	Gly	Ala	Tyr	Arg	Glu	Ser	Thr	Glu	Phe		

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165 170 175
 Ile Lys Ser Thr Leu Lys Leu Trp Arg Lys Val Phe Lys Arg Lys Phe
 180 185 190
 Lys Val Val Ile Thr Gly Gly Glu Gly Lys Tyr Phe Ser Lys Phe Gly
 195 200 205
 Ile Tyr Asp Pro Leu Leu Val His Arg Gly Met Arg Asn Leu Leu Tyr
 210 215 220
 Leu Tyr His Arg Ile
 225

<210> 16

<211> 257

<212> PRT

<213> Synechocystis sp.

<400> 16

Met Glu Thr Ser Lys Pro Gly Cys Gly Leu Ala Leu Asp Asn Asp Lys
 1 5 10 15
 Gln Lys Pro Trp Leu Gly Leu Met Ile Gly Asn Ser Arg Leu His Trp
 20 25 30
 Ala Tyr Cys Ser Gly Asn Ala Pro Leu Gln Thr Trp Val Thr Asp Tyr
 35 40 45
 Asn Pro Lys Ser Ala Gln Leu Pro Val Leu Leu Gly Lys Val Pro Leu
 50 55 60
 Met Leu Ala Ser Val Val Pro Glu Gln Thr Glu Val Trp Arg Val Tyr
 65 70 75 80
 Gln Pro Lys Ile Leu Thr Leu Lys Asn Leu Pro Leu Val Asn Leu Tyr
 85 90 95
 Pro Ser Phe Gly Ile Asp Arg Ala Leu Ala Gly Leu Gly Thr Gly Leu
 100 105 110
 Thr Tyr Gly Phe Pro Cys Leu Val Val Asp Gly Gly Thr Ala Leu Thr
 115 120 125
 Ile Thr Gly Phe Asp Gln Asp Lys Lys Leu Val Gly Gly Ala Ile Leu
 130 135 140
 Pro Gly Leu Gly Leu Gln Leu Ala Thr Leu Gly Asp Arg Leu Ala Ala
 145 150 155 160
 Leu Pro Lys Leu Glu Met Asp Gln Leu Thr Glu Leu Pro Asp Arg Trp
 165 170 175
 Ala Leu Asp Thr Pro Ser Ala Ile Phe Ser Gly Val Val Tyr Gly Val
 180 185 190
 Leu Gly Ala Leu Gln Ser Tyr Leu Gln Asp Trp Gln Lys Leu Phe Pro

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195	200	205
Gly Ala Ala Met Val Ile Thr Gly Gly Asp Gly Lys Ile Leu His Gly		
210	215	220
Phe Leu Lys Glu His Ser Pro Asn Leu Ser Val Ala Trp Asp Asp Asn		
225	230	235
Leu Ile Phe Leu Gly Met Ala Ala Ile His His Gly Asp Arg Pro Ile		
	245	250
		255
Cys		

<210> 17

<211> 223

<212> PRT

<213> Helicobacter pylori

<400> 17

Met Pro Ala Arg Gln Ser Phe Thr Asp Leu Lys Asn Leu Val Leu Cys
1 5 10 15
Asp Ile Gly Asn Thr Arg Ile His Phe Ala Gln Asn Tyr Gln Leu Phe
20 25 30
Ser Ser Ala Lys Glu Asp Leu Lys Arg Leu Gly Ile Gln Lys Glu Ile
35 40 45
Phe Tyr Ile Ser Val Asn Glu Glu Asn Glu Lys Ala Leu Leu Asn Cys
50 55 60
Tyr Pro Asn Ala Lys Asn Ile Ala Gly Phe Phe His Leu Glu Thr Asp
65 70 75 80
Tyr Val Gly Leu Gly Ile Asp Arg Gln Met Ala Cys Leu Ala Val Asn
85 90 95
Asn Gly Val Val Val Asp Ala Gly Ser Ala Ile Thr Ile Asp Leu Ile
100 105 110
Lys Glu Gly Lys His Leu Gly Gly Cys Ile Leu Pro Gly Leu Ala Gln
115 120 125
Tyr Ile His Ala Tyr Lys Lys Ser Ala Lys Ile Leu Glu Gln Pro Phe
130 135 140
Lys Ala Leu Asp Ser Leu Glu Val Leu Pro Lys Ser Thr Arg Asp Ala
145 150 155 160
Val Asn Tyr Gly Met Val Leu Ser Val Ile Ala Cys Ile Gln His Leu
165 170 175
Ala Lys Asn Gln Lys Ile Tyr Leu Cys Gly Gly Asp Ala Lys Tyr Leu
180 185 190
Ser Ala Phe Leu Pro His Ser Val Cys Lys Glu Arg Leu Val Phe Asp

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195 200 205
 Gly Met Glu Ile Ala Leu Lys Lys Ala Gly Ile Leu Glu Cys Lys
 210 215 220

<210> 18
 <211> 267
 <212> PRT
 <213> Bordetella pertussis

<400> 18
 Met Ile Ile Leu Ile Asp Ser Gly Asn Ser Arg Leu Lys Val Gly Trp
 1 5 10 15

Phe Asp Pro Asp Ala Pro Gln Ala Ala Arg Glu Pro Ala Pro Val Ala
 20 25 30

Phe Asp Asn Leu Asp Leu Asp Ala Leu Gly Arg Trp Leu Ala Thr Leu
 35 40 45

Pro Arg Arg Pro Gln Arg Ala Leu Gly Val Asn Val Ala Gly Leu Ala
 50 55 60

Arg Gly Glu Ala Ile Ala Ala Thr Leu Arg Ala Gly Gly Cys Asp Ile
 65 70 75 80

Arg Trp Leu Arg Ala Gln Pro Leu Ala Met Gly Leu Arg Asn Gly Tyr
 85 90 95

Arg Asn Pro Asp Gln Leu Gly Ala Asp Arg Trp Ala Cys Met Val Gly
 100 105 110

Val Leu Ala Arg Gln Pro Ser Val His Pro Pro Leu Leu Val Ala Ser
 115 120 125

Phe Gly Thr Ala Thr Thr Leu Asp Thr Ile Gly Pro Asp Asn Val Phe
 130 135 140

Pro Gly Gly Leu Ile Leu Pro Gly Pro Ala Met Met Arg Gly Ala Leu
 145 150 155 160

Ala Tyr Gly Thr Ala His Leu Pro Leu Ala Asp Gly Leu Val Ala Asp
 165 170 175

Tyr Pro Ile Asp Thr His Gln Ala Ile Ala Ser Gly Ile Ala Ala Ala
 180 185 190

Gln Ala Gly Ala Ile Val Arg Gln Trp Leu Ala Gly Arg Gln Arg Tyr
 195 200 205

Gly Gln Ala Pro Glu Ile Tyr Val Ala Gly Gly Gly Trp Pro Glu Val
 210 215 220

Arg Gln Glu Ala Glu Arg Leu Leu Ala Val Thr Gly Ala Ala Phe Gly
 225 230 235 240

Ala Thr Pro Gln Pro Thr Tyr Leu Asp Ser Pro Val Leu Asp Gly Leu

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245 250 255
 Ala Ala Leu Ala Ala Gln Gly Ala Pro Thr Ala
 260 265

<210> 19
 <211> 777
 <212> DNA
 <213> Bacillus subtilis
 <220>
 <221> CDS
 <222> (1)..(774)

<400> 19
 ttg tta ctg gtt atc gat gtg ggg aac acc aat act gta ctt ggt gta 48
 Leu Leu Leu Val Ile Asp Val Gly Asn Thr Asn Thr Val Leu Gly Val
 1 5 10 15
 tat cat gat gga aaa tta gaa tat cac tgg cgt ata gaa aca agc agg 96
 Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg
 20 25 30
 cat aaa aca gaa gat gag ttt ggg atg att ttg cgc tcc tta ttt gat 144
 His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Phe Asp
 35 40 45
 cac tcc ggg ctt atg ttt gaa cag ata gat ggc att att att tcg tca 192
 His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser
 50 55 60
 gta gtg ccg cca atc atg ttt gcg tta gaa aga atg tgc aca aaa tac 240
 Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Thr Lys Tyr
 65 70 75 80
 ttt cat atc gag cct caa att gtt ggt cca ggt atg aaa acc ggt tta 288
 Phe His Ile Glu Pro Gln Ile Val Gly Pro Gly Met Lys Thr Gly Leu
 85 90 95
 aat ata aaa tat gac aat ccg aaa gaa gta ggg gca gac aga atc gta 336
 Asn Ile Lys Tyr Asp Asn Pro Lys Glu Val Gly Ala Asp Arg Ile Val
 100 105 110
 aat gct gtc gct gcg ata cac ttg tac ggc aat cca tta att gtt gtc 384
 Asn Ala Val Ala Ala Ile His Leu Tyr Gly Asn Pro Leu Ile Val Val
 115 120 125
 gat ttc gga acc gcc aca acg tac tgc tat att gat gaa aac aaa caa 432
 Asp Phe Gly Thr Ala Thr Thr Tyr Cys Tyr Ile Asp Glu Asn Lys Gln
 130 135 140
 tac atg ggc ggg gcg att gcc cct ggg att aca att tcg aca gag gcg 480
 Tyr Met Gly Gly Ala Ile Ala Pro Gly Ile Thr Ile Ser Thr Glu Ala
 145 150 155 160
 ctt tac tcg cgt gca gca aag ctt cct cgt atc gaa atc acc cgg ccc 528
 Leu Tyr Ser Arg Ala Ala Lys Leu Pro Arg Ile Glu Ile Thr Arg Pro

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				165					170					175			
gac	aat	att	atc	gga	aaa	aac	act	gtt	agc	gcg	atg	caa	tct	gga	att		576
Asp	Asn	Ile	Ile	Gly	Lys	Asn	Thr	Val	Ser	Ala	Met	Gln	Ser	Gly	Ile		
			180					185					190				
tta	ttt	ggc	tat	gtc	ggc	caa	gtg	gaa	gga	atc	gtt	aag	cga	atg	aaa		624
Leu	Phe	Gly	Tyr	Val	Gly	Gln	Val	Glu	Gly	Ile	Val	Lys	Arg	Met	Lys		
		195					200					205					
tgg	cag	gca	aaa	cag	gac	ctc	aag	gtc	att	gcg	aca	gga	ggc	ctg	gcg		672
Trp	Gln	Ala	Lys	Gln	Asp	Leu	Lys	Val	Ile	Ala	Thr	Gly	Gly	Leu	Ala		
	210					215					220						
ccg	ctc	att	gcg	aac	gaa	tca	gat	tgt	ata	gac	atc	gtt	gat	cca	ttc		720
Pro	Leu	Ile	Ala	Asn	Glu	Ser	Asp	Cys	Ile	Asp	Ile	Val	Asp	Pro	Phe		
	225				230					235					240		
tta	acc	cta	aaa	ggg	ctg	gaa	ttg	att	tat	gaa	aga	aac	cgc	gta	gga		768
Leu	Thr	Leu	Lys	Gly	Leu	Glu	Leu	Ile	Tyr	Glu	Arg	Asn	Arg	Val	Gly		
				245				250						255			
agt	gta	tag															777
Ser	Val																

<210> 20

<211> 960

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(957)

<400> 20

gtg	aaa	aat	aaa	gaa	ctt	aac	cta	cat	act	tta	tat	aca	cag	cac	aat		48
Met	Lys	Asn	Lys	Glu	Leu	Asn	Leu	His	Thr	Leu	Tyr	Thr	Gln	His	Asn		
1				5				10					15				
cgg	gag	tct	tgg	tct	ggt	ttt	ggg	ggg	cat	ttg	tcg	att	gct	gta	tct		96
Arg	Glu	Ser	Trp	Ser	Gly	Phe	Gly	Gly	His	Leu	Ser	Ile	Ala	Val	Ser		
			20				25						30				
gaa	gaa	gag	gca	aaa	gct	gtg	gaa	gga	ttg	aat	gat	tat	cta	tct	gtt		144
Glu	Glu	Glu	Ala	Lys	Ala	Val	Glu	Gly	Leu	Asn	Asp	Tyr	Leu	Ser	Val		
		35				40						45					
gaa	gaa	gtg	gag	acg	atc	tat	att	ccg	ctt	gtt	cgc	ttg	ctt	cat	tta		192
Glu	Glu	Val	Glu	Thr	Ile	Tyr	Ile	Pro	Leu	Val	Arg	Leu	Leu	His	Leu		
	50				55						60						
cat	gtc	aag	tct	gcg	gct	gaa	cgc	aat	aag	cat	gtc	aat	gtt	ttt	ttg		240
His	Val	Lys	Ser	Ala	Ala	Glu	Arg	Asn	Lys	His	Val	Asn	Val	Phe	Leu		
	65			70				75						80			
aag	cac	cca	cat	tca	gcc	aaa	att	ccg	ttt	att	atc	ggc	att	gcc	ggc		288
Lys	His	Pro	His	Ser	Ala	Lys	Ile	Pro	Phe	Ile	Ile	Gly	Ile	Ala	Gly		

85							90							95			
agt	gtc	gca	gtc	gga	aaa	agc	acg	acg	gcg	cgg	atc	ttg	cag	aag	ctg		336
Ser	Val	Ala	Val	Gly	Lys	Ser	Thr	Thr	Ala	Arg	Ile	Leu	Gln	Lys	Leu		
			100					105					110				
ctt	tcg	cgt	ttg	cct	gac	cgt	cca	aaa	gtg	agc	ctt	atc	acg	aca	gat		384
Leu	Ser	Arg	Leu	Pro	Asp	Arg	Pro	Lys	Val	Ser	Leu	Ile	Thr	Thr	Asp		
		115					120					125					
ggt	ttt	tta	ttt	cct	act	gcc	gag	ctg	aaa	aag	aaa	aat	atg	atg	tca		432
Gly	Phe	Leu	Phe	Pro	Thr	Ala	Glu	Leu	Lys	Lys	Lys	Asn	Met	Met	Ser		
	130					135					140						
aga	aaa	gga	ttt	cct	gaa	agc	tat	gat	gta	aag	gcg	ctg	ctc	gaa	ttt		480
Arg	Lys	Gly	Phe	Pro	Glu	Ser	Tyr	Asp	Val	Lys	Ala	Leu	Leu	Glu	Phe		
145					150					155					160		
ttg	aat	gac	tta	aaa	tca	gga	aag	gac	agc	gta	aag	gcc	ccg	gtg	tat		528
Leu	Asn	Asp	Leu	Lys	Ser	Gly	Lys	Asp	Ser	Val	Lys	Ala	Pro	Val	Tyr		
				165				170						175			
tcc	cat	cta	acc	tat	gac	cgc	gag	gaa	ggt	gtg	ttc	gag	ggt	gta	gaa		576
Ser	His	Leu	Thr	Tyr	Asp	Arg	Glu	Glu	Gly	Val	Phe	Glu	Val	Val	Glu		
			180					185					190				
cag	gcg	gat	att	gtg	att	att	gaa	ggc	att	aat	ggt	ctt	cag	tcg	ccc		624
Gln	Ala	Asp	Ile	Val	Ile	Ile	Glu	Gly	Ile	Asn	Val	Leu	Gln	Ser	Pro		
		195					200					205					
acc	ttg	gag	gat	gac	cgg	gaa	aac	ccg	cgt	att	ttt	ggt	tcc	gat	ttc		672
Thr	Leu	Glu	Asp	Asp	Arg	Glu	Asn	Pro	Arg	Ile	Phe	Val	Ser	Asp	Phe		
	210					215					220						
ttt	gat	ttt	tcg	att	tat	gtg	gat	gcg	gag	gaa	agc	cgg	att	ttc	act		720
Phe	Asp	Phe	Ser	Ile	Tyr	Val	Asp	Ala	Glu	Glu	Ser	Arg	Ile	Phe	Thr		
225					230					235					240		
tgg	tat	tta	gag	cgt	ttt	cgc	ctg	ctt	cgg	gaa	aca	gct	ttt	caa	aat		768
Trp	Tyr	Leu	Glu	Arg	Phe	Arg	Leu	Leu	Arg	Glu	Thr	Ala	Phe	Gln	Asn		
				245				250					255				
cct	gat	tca	tat	ttt	cat	aaa	ttt	aaa	gac	ttg	tcc	gat	cag	gag	gct		816
Pro	Asp	Ser	Tyr	Phe	His	Lys	Phe	Lys	Asp	Leu	Ser	Asp	Gln	Glu	Ala		
			260					265					270				
gac	gag	atg	gca	gcc	tcg	att	tgg	gag	agt	gtc	aac	cgg	ccg	aat	tta		864
Asp	Glu	Met	Ala	Ala	Ser	Ile	Trp	Glu	Ser	Val	Asn	Arg	Pro	Asn	Leu		
		275					280					285					
tat	gaa	aat	att	ttg	cca	act	aaa	ttc	agg	tca	gat	ctc	att	ttg	cgt		912
Tyr	Glu	Asn	Ile	Leu	Pro	Thr	Lys	Phe	Arg	Ser	Asp	Leu	Ile	Leu	Arg		
	290					295					300						
aag	gga	gac	ggg	cat	aag	gtc	gag	gaa	gtg	ttg	gta	agg	agg	gta	tga		960
Lys	Gly	Asp	Gly	His	Lys	Val	Glu	Glu	Val	Leu	Val	Arg	Arg	Val			
305					310					315							

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<210> 21
 <211> 882
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(879)

<400> 21
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 Met Ser Ile Ala Val Ser Glu Glu Glu Ala Lys Ala Val Glu Gly Leu
 1 5 10 15
 aat gat tat cta tct gtt gaa gaa gtg gag acg atc tat att ccg ctt 96
 Asn Asp Tyr Leu Ser Val Glu Glu Val Glu Thr Ile Tyr Ile Pro Leu
 20 25 30
 gtt cgc ttg ctt cat tta cat gtc aag tct gcg gct gaa cgc aat aag 144
 Val Arg Leu Leu His Leu His Val Lys Ser Ala Ala Glu Arg Asn Lys
 35 40 45
 cat gtc aat gtt ttt ttg aag cac cca cat tca gcc aaa att ccg ttt 192
 His Val Asn Val Phe Leu Lys His Pro His Ser Ala Lys Ile Pro Phe
 50 55 60
 att atc ggc att gcc ggc agt gtc gca gtc gga aaa agc acg acg gcg 240
 Ile Ile Gly Ile Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala
 65 70 75 80
 cgg atc ttg cag aag ctg ctt tcg cgt ttg cct gac cgt cca aaa gtg 288
 Arg Ile Leu Gln Lys Leu Leu Ser Arg Leu Pro Asp Arg Pro Lys Val
 85 90 95
 agc ctt atc acg aca gat ggt ttt tta ttt cct act gcc gag ctg aaa 336
 Ser Leu Ile Thr Thr Asp Gly Phe Leu Phe Pro Thr Ala Glu Leu Lys
 100 105 110
 aag aaa aat atg atg tca aga aaa gga ttt cct gaa agc tat gat gta 384
 Lys Lys Asn Met Met Ser Arg Lys Gly Phe Pro Glu Ser Tyr Asp Val
 115 120 125
 aag gcg ctg ctc gaa ttt ttg aat gac tta aaa tca gga aag gac agc 432
 Lys Ala Leu Leu Glu Phe Leu Asn Asp Leu Lys Ser Gly Lys Asp Ser
 130 135 140
 gta aag gcc ccg gtg tat tcc cat cta acc tat gac cgc gag gaa ggt 480
 Val Lys Ala Pro Val Tyr Ser His Leu Thr Tyr Asp Arg Glu Glu Gly
 145 150 155 160
 gtg ttc gag gtt gta gaa cag gcg gat att gtg att att gaa ggc att 528
 Val Phe Glu Val Val Glu Gln Ala Asp Ile Val Ile Ile Glu Gly Ile
 165 170 175
 aat gtt ctt cag tcg ccc acc ttg gag gat gac cgg gaa aac ccg cgt 576
 Asn Val Leu Gln Ser Pro Thr Leu Glu Asp Asp Arg Glu Asn Pro Arg
 180 185 190

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att ttt gtt tcc gat ttc ttt gat ttt tcg att tat gtg gat gcg gag	624
Ile Phe Val Ser Asp Phe Phe Asp Phe Ser Ile Tyr Val Asp Ala Glu	
195 200 205	
gaa agc cgg att ttc act tgg tat tta gag cgt ttt cgc ctg ctt cgg	672
Glu Ser Arg Ile Phe Thr Trp Tyr Leu Glu Arg Phe Arg Leu Leu Arg	
210 215 220	
gaa aca gct ttt caa aat cct gat tca tat ttt cat aaa ttt aaa gac	720
Glu Thr Ala Phe Gln Asn Pro Asp Ser Tyr Phe His Lys Phe Lys Asp	
225 230 235 240	
ttg tcc gat cag gag gct gac gag atg gca gcc tcg att tgg gag agt	768
Leu Ser Asp Gln Glu Ala Asp Glu Met Ala Ala Ser Ile Trp Glu Ser	
245 250 255	
gtc aac cgg ccg aat tta tat gaa aat att ttg cca act aaa ttc agg	816
Val Asn Arg Pro Asn Leu Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg	
260 265 270	
tca gat ctc att ttg cgt aag gga gac ggg cat aag gtc gag gaa gtg	864
Ser Asp Leu Ile Leu Arg Lys Gly Asp Gly His Lys Val Glu Glu Val	
275 280 285	
ttg gta agg agg gta tga	882
Leu Val Arg Arg Val	
290	

<210> 22
 <211> 846
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(843)

<400> 22	
gtg gaa gga ttg aat gat tat cta tct gtt gaa gaa gtg gag acg atc	48
Met Glu Gly Leu Asn Asp Tyr Leu Ser Val Glu Glu Val Glu Thr Ile	
1 5 10 15	
tat att ccg ctt gtt cgc ttg ctt cat tta cat gtc aag tct gcg gct	96
Tyr Ile Pro Leu Val Arg Leu Leu His Leu His Val Lys Ser Ala Ala	
20 25 30	
gaa cgc aat aag cat gtc aat gtt ttt ttg aag cac cca cat tca gcc	144
Glu Arg Asn Lys His Val Asn Val Phe Leu Lys His Pro His Ser Ala	
35 40 45	
aaa att ccg ttt att atc ggc att gcc ggc agt gtc gca gtc gga aaa	192
Lys Ile Pro Phe Ile Ile Gly Ile Ala Gly Ser Val Ala Val Gly Lys	
50 55 60	
agc acg acg gcg cgg atc ttg cag aag ctg ctt tcg cgt ttg cct gac	240
Ser Thr Thr Ala Arg Ile Leu Gln Lys Leu Leu Ser Arg Leu Pro Asp	

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65					70						75					80	
cgt	cca	aaa	gtg	agc	ctt	atc	acg	aca	gat	ggt	ttt	tta	ttt	cct	act		288
Arg	Pro	Lys	Val	Ser	Leu	Ile	Thr	Thr	Asp	Gly	Phe	Leu	Phe	Pro	Thr		
				85					90					95			
gcc	gag	ctg	aaa	aag	aaa	aat	atg	atg	tca	aga	aaa	gga	ttt	cct	gaa		336
Ala	Glu	Leu	Lys	Lys	Lys	Asn	Met	Met	Ser	Arg	Lys	Gly	Phe	Pro	Glu		
			100					105					110				
agc	tat	gat	gta	aag	gcg	ctg	ctc	gaa	ttt	ttg	aat	gac	tta	aaa	tca		384
Ser	Tyr	Asp	Val	Lys	Ala	Leu	Leu	Glu	Phe	Leu	Asn	Asp	Leu	Lys	Ser		
		115				120						125					
gga	aag	gac	agc	gta	aag	gcc	ccg	gtg	tat	tcc	cat	cta	acc	tat	gac		432
Gly	Lys	Asp	Ser	Val	Lys	Ala	Pro	Val	Tyr	Ser	His	Leu	Thr	Tyr	Asp		
	130					135					140						
cgc	gag	gaa	ggt	gtg	ttc	gag	ggt	gta	gaa	cag	gcg	gat	att	gtg	att		480
Arg	Glu	Glu	Gly	Val	Phe	Glu	Val	Val	Glu	Gln	Ala	Asp	Ile	Val	Ile		
145					150					155				160			
att	gaa	ggc	att	aat	gtt	ctt	cag	tcg	ccc	acc	ttg	gag	gat	gac	cgg		528
Ile	Glu	Gly	Ile	Asn	Val	Leu	Gln	Ser	Pro	Thr	Leu	Glu	Asp	Asp	Arg		
				165					170					175			
gaa	aac	ccg	cgt	att	ttt	gtt	tcc	gat	ttc	ttt	gat	ttt	tcg	att	tat		576
Glu	Asn	Pro	Arg	Ile	Phe	Val	Ser	Asp	Phe	Phe	Asp	Phe	Ser	Ile	Tyr		
			180					185					190				
gtg	gat	gcg	gag	gaa	agc	cgg	att	ttc	act	tgg	tat	tta	gag	cgt	ttt		624
Val	Asp	Ala	Glu	Glu	Ser	Arg	Ile	Phe	Thr	Trp	Tyr	Leu	Glu	Arg	Phe		
		195				200						205					
cgc	ctg	ctt	cgg	gaa	aca	gct	ttt	caa	aat	cct	gat	tca	tat	ttt	cat		672
Arg	Leu	Leu	Arg	Glu	Thr	Ala	Phe	Gln	Asn	Pro	Asp	Ser	Tyr	Phe	His		
	210					215					220						
aaa	ttt	aaa	gac	ttg	tcc	gat	cag	gag	gct	gac	gag	atg	gca	gcc	tcg		720
Lys	Phe	Lys	Asp	Leu	Ser	Asp	Gln	Glu	Ala	Asp	Glu	Met	Ala	Ala	Ser		
225				230						235				240			
att	tgg	gag	agt	gtc	aac	cgg	ccg	aat	tta	tat	gaa	aat	att	ttg	cca		768
Ile	Trp	Glu	Ser	Val	Asn	Arg	Pro	Asn	Leu	Tyr	Glu	Asn	Ile	Leu	Pro		
				245				250					255				
act	aaa	ttc	agg	tca	gat	ctc	att	ttg	cgt	aag	gga	gac	ggg	cat	aag		816
Thr	Lys	Phe	Arg	Ser	Asp	Leu	Ile	Leu	Arg	Lys	Gly	Asp	Gly	His	Lys		
			260			265						270					
gtc	gag	gaa	gtg	ttg	gta	agg	agg	gta	tga								846
Val	Glu	Glu	Val	Leu	Val	Arg	Arg	Val									
		275				280											

<210> 23

<211> 831

<212> DNA

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<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(831)

<400> 23

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Met	Lys	Thr	Lys	Leu	Asp	Phe	Leu	Lys	Met	Lys	Glu	Ser	Glu	Glu	Pro	
1				5					10					15		
att	gtc	atg	ctg	acc	gct	tat	gat	tat	ccg	gca	gct	aaa	ctt	gct	gaa	96
Ile	Val	Met	Leu	Thr	Ala	Tyr	Asp	Tyr	Pro	Ala	Ala	Lys	Leu	Ala	Glu	
			20					25					30			
caa	gcg	gga	gtt	gac	atg	att	tta	gtc	ggt	gat	tca	ctt	gga	atg	gtc	144
Gln	Ala	Gly	Val	Asp	Met	Ile	Leu	Val	Gly	Asp	Ser	Leu	Gly	Met	Val	
		35					40					45				
gtc	ctc	ggc	ctt	gat	tca	act	gtc	ggt	gtg	aca	gtt	gcg	gac	atg	atc	192
Val	Leu	Gly	Leu	Asp	Ser	Thr	Val	Gly	Val	Thr	Val	Ala	Asp	Met	Ile	
	50					55					60					
cat	cat	aca	aaa	gcc	gtt	aaa	agg	ggt	gcg	ccg	aat	acc	ttt	att	gtg	240
His	His	Thr	Lys	Ala	Val	Lys	Arg	Gly	Ala	Pro	Asn	Thr	Phe	Ile	Val	
65					70				75						80	
aca	gat	atg	ccg	ttt	atg	tct	tat	cac	ctg	tct	aag	gaa	gat	acg	ctg	288
Thr	Asp	Met	Pro	Phe	Met	Ser	Tyr	His	Leu	Ser	Lys	Glu	Asp	Thr	Leu	
				85					90					95		
aaa	aat	gca	gcg	gct	atc	gtt	cag	gaa	agc	gga	gct	gac	gca	ctg	aag	336
Lys	Asn	Ala	Ala	Ala	Ile	Val	Gln	Glu	Ser	Gly	Ala	Asp	Ala	Leu	Lys	
			100					105					110			
ctt	gag	ggc	gga	gaa	ggc	gtg	ttt	gaa	tcc	att	cgc	gca	ttg	acg	ctt	384
Leu	Glu	Gly	Gly	Glu	Gly	Val	Phe	Glu	Ser	Ile	Arg	Ala	Leu	Thr	Leu	
		115					120					125				
gga	ggc	att	cca	gta	gtc	agt	cac	tta	ggt	ttg	aca	ccg	cag	tca	gtc	432
Gly	Gly	Ile	Pro	Val	Val	Ser	His	Leu	Gly	Leu	Thr	Pro	Gln	Ser	Val	
	130					135					140					
ggc	gta	ctg	ggc	ggc	tat	aaa	gta	cag	ggc	aaa	gac	gaa	caa	agc	gcc	480
Gly	Val	Leu	Gly	Gly	Tyr	Lys	Val	Gln	Gly	Lys	Asp	Glu	Gln	Ser	Ala	
145					150					155					160	
aaa	aaa	tta	ata	gaa	gac	agt	ata	aaa	tgc	gaa	gaa	gca	gga	gct	atg	528
Lys	Lys	Leu	Ile	Glu	Asp	Ser	Ile	Lys	Cys	Glu	Glu	Ala	Gly	Ala	Met	
				165					170					175		
atg	ctt	gtg	ctg	gaa	tgt	gtg	ccg	gca	gaa	ctc	aca	gcc	aaa	att	gcc	576
Met	Leu	Val	Leu	Glu	Cys	Val	Pro	Ala	Glu	Leu	Thr	Ala	Lys	Ile	Ala	
			180					185					190			
gag	acg	cta	agc	ata	ccg	gtc	att	gga	atc	ggg	gct	ggt	gtg	aaa	gcg	624
Glu	Thr	Leu	Ser	Ile	Pro	Val	Ile	Gly	Ile	Gly	Ala	Gly	Val	Lys	Ala	
		195				200						205				

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gac gga caa gtt ctc gtt tat cat gat att atc ggc cac ggt gtt gag	672
Asp Gly Gln Val Leu Val Tyr His Asp Ile Ile Gly His Gly Val Glu	
210 215 220	
aga aca cct aaa ttt gta aag caa tat acg cgc att gat gaa acc atc	720
Arg Thr Pro Lys Phe Val Lys Gln Tyr Thr Arg Ile Asp Glu Thr Ile	
225 230 235 240	
gaa aca gca atc agc gga tat gtt cag gat gta aga cat cgt gct ttc	768
Glu Thr Ala Ile Ser Gly Tyr Val Gln Asp Val Arg His Arg Ala Phe	
245 250 255	
cct gaa caa aag cat tcc ttt caa atg aac cag aca gtg ctt gac ggc	816
Pro Glu Gln Lys His Ser Phe Gln Met Asn Gln Thr Val Leu Asp Gly	
260 265 270	
ttg tac ggg gga aaa	831
Leu Tyr Gly Gly Lys	
275	

<210> 24

<211> 277

<212> PRT

<213> Bacillus subtilis

<400> 24

Met Lys Thr Lys Leu Asp Phe Leu Lys Met Lys Glu Ser Glu Glu Pro	
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Ile Val Met Leu Thr Ala Tyr Asp Tyr Pro Ala Ala Lys Leu Ala Glu	
20 25 30	
Gln Ala Gly Val Asp Met Ile Leu Val Gly Asp Ser Leu Gly Met Val	
35 40 45	
Val Leu Gly Leu Asp Ser Thr Val Gly Val Thr Val Ala Asp Met Ile	
50 55 60	
His His Thr Lys Ala Val Lys Arg Gly Ala Pro Asn Thr Phe Ile Val	
65 70 75 80	
Thr Asp Met Pro Phe Met Ser Tyr His Leu Ser Lys Glu Asp Thr Leu	
85 90 95	
Lys Asn Ala Ala Ala Ile Val Gln Glu Ser Gly Ala Asp Ala Leu Lys	
100 105 110	
Leu Glu Gly Gly Glu Gly Val Phe Glu Ser Ile Arg Ala Leu Thr Leu	
115 120 125	
Gly Gly Ile Pro Val Val Ser His Leu Gly Leu Thr Pro Gln Ser Val	
130 135 140	
Gly Val Leu Gly Gly Tyr Lys Val Gln Gly Lys Asp Glu Gln Ser Ala	
145 150 155 160	

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Lys	Lys	Leu	Ile	Glu	Asp	Ser	Ile	Lys	Cys	Glu	Glu	Ala	Gly	Ala	Met	
				165					170					175		
Met	Leu	Val	Leu	Glu	Cys	Val	Pro	Ala	Glu	Leu	Thr	Ala	Lys	Ile	Ala	
			180					185					190			
Glu	Thr	Leu	Ser	Ile	Pro	Val	Ile	Gly	Ile	Gly	Ala	Gly	Val	Lys	Ala	
		195					200					205				
Asp	Gly	Gln	Val	Leu	Val	Tyr	His	Asp	Ile	Ile	Gly	His	Gly	Val	Glu	
	210					215					220					
Arg	Thr	Pro	Lys	Phe	Val	Lys	Gln	Tyr	Thr	Arg	Ile	Asp	Glu	Thr	Ile	
	225				230					235					240	
Glu	Thr	Ala	Ile	Ser	Gly	Tyr	Val	Gln	Asp	Val	Arg	His	Arg	Ala	Phe	
				245					250					255		
Pro	Glu	Gln	Lys	His	Ser	Phe	Gln	Met	Asn	Gln	Thr	Val	Leu	Asp	Gly	
			260					265					270			
Leu	Tyr	Gly	Gly	Lys												
		275														

<210> 25
 <211> 858
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(858)

<400> 25																	
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Met	Arg	Gln	Ile	Thr	Asp	Ile	Ser	Gln	Leu	Lys	Glu	Ala	Ile	Lys	Gln		
1				5					10					15			
tac	cat	tca	gag	ggc	aag	tca	atc	gga	ttt	gtt	ccg	acg	atg	ggg	ttt		96
Tyr	His	Ser	Glu	Gly	Lys	Ser	Ile	Gly	Phe	Val	Pro	Thr	Met	Gly	Phe		
			20					25					30				
ctg	cat	gag	ggg	cat	tta	acc	tta	gca	gac	aaa	gca	aga	caa	gaa	aac		144
Leu	His	Glu	Gly	His	Leu	Thr	Leu	Ala	Asp	Lys	Ala	Arg	Gln	Glu	Asn		
			35				40					45					
gac	gcc	gtt	att	atg	agt	att	ttt	gtg	aat	cct	gca	caa	ttc	ggc	cct		192
Asp	Ala	Val	Ile	Met	Ser	Ile	Phe	Val	Asn	Pro	Ala	Gln	Phe	Gly	Pro		
	50					55				60							
aat	gaa	gat	ttt	gaa	gca	tat	ccg	cgc	gat	att	gag	cgg	gat	gca	gct		240
Asn	Glu	Asp	Phe	Glu	Ala	Tyr	Pro	Arg	Asp	Ile	Glu	Arg	Asp	Ala	Ala		
65				70					75					80			
ctt	gca	gaa	aac	gcc	gga	gtc	gat	att	ctt	ttt	acg	cca	gat	gct	cat		288
Leu	Ala	Glu	Asn	Ala	Gly	Val	Asp	Ile	Leu	Phe	Thr	Pro	Asp	Ala	His		
				85					90					95			

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gat	atg	tat	ccc	ggt	gaa	aag	aat	gtc	acg	att	cat	gta	gaa	aga	cgc	336
Asp	Met	Tyr	Pro	Gly	Glu	Lys	Asn	Val	Thr	Ile	His	Val	Glu	Arg	Arg	
			100					105					110			
aca	gac	gtg	tta	tgc	ggg	cgc	tca	aga	gaa	gga	cat	ttt	gac	ggg	gtc	384
Thr	Asp	Val	Leu	Cys	Gly	Arg	Ser	Arg	Glu	Gly	His	Phe	Asp	Gly	Val	
		115					120					125				
gcg	atc	gta	ctg	acg	aag	ctt	ttc	aat	cta	gtc	aag	ccg	act	cgt	gcc	432
Ala	Ile	Val	Leu	Thr	Lys	Leu	Phe	Asn	Leu	Val	Lys	Pro	Thr	Arg	Ala	
	130					135					140					
tat	ttc	ggt	tta	aaa	gat	gcg	cag	cag	gta	gct	gtt	gtt	gat	ggg	tta	480
Tyr	Phe	Gly	Leu	Lys	Asp	Ala	Gln	Gln	Val	Ala	Val	Val	Asp	Gly	Leu	
					150					155					160	
atc	agc	gac	ttc	ttc	atg	gat	att	gaa	ttg	gtt	cct	gtc	gat	acg	gtc	528
Ile	Ser	Asp	Phe	Phe	Met	Asp	Ile	Glu	Leu	Val	Pro	Val	Asp	Thr	Val	
				165					170					175		
aga	gag	gaa	gac	ggc	tta	gcc	aaa	agc	tct	cgc	aat	gta	tac	tta	aca	576
Arg	Glu	Glu	Asp	Gly	Leu	Ala	Lys	Ser	Ser	Arg	Asn	Val	Tyr	Leu	Thr	
			180					185					190			
gct	gag	gaa	aga	aaa	gaa	gcg	cct	aag	ctg	tat	cgg	gcc	ctt	caa	aca	624
Ala	Glu	Glu	Arg	Lys	Glu	Ala	Pro	Lys	Leu	Tyr	Arg	Ala	Leu	Gln	Thr	
		195					200					205				
agt	gcg	gaa	ctt	gtc	caa	gcc	ggt	gaa	aga	gat	cct	gaa	gcg	gtg	ata	672
Ser	Ala	Glu	Leu	Val	Gln	Ala	Gly	Glu	Arg	Asp	Pro	Glu	Ala	Val	Ile	
	210					215					220					
aaa	gct	gca	aaa	gat	atc	att	gaa	acg	act	agc	gga	acc	ata	gac	tat	720
Lys	Ala	Ala	Lys	Asp	Ile	Ile	Glu	Thr	Thr	Ser	Gly	Thr	Ile	Asp	Tyr	
	225				230					235					240	
gta	gag	ctt	tat	tcc	tat	ccg	gaa	ctc	gag	cct	gtg	aat	gaa	att	gct	768
Val	Glu	Leu	Tyr	Ser	Tyr	Pro	Glu	Leu	Glu	Pro	Val	Asn	Glu	Ile	Ala	
				245					250					255		
gga	aag	atg	att	ctc	gct	gtt	gca	gtt	gct	ttt	tca	aaa	gcg	cgt	tta	816
Gly	Lys	Met	Ile	Leu	Ala	Val	Ala	Val	Ala	Phe	Ser	Lys	Ala	Arg	Leu	
			260					265					270			
ata	gat	aat	atc	att	att	gat	att	cga	gaa	atg	gag	aga	ata			858
Ile	Asp	Asn	Ile	Ile	Ile	Asp	Ile	Arg	Glu	Met	Glu	Arg	Ile			
		275					280					285				

<210> 26

<211> 286

<212> PRT

<213> Bacillus subtilis

<400> 26

Met	Arg	Gln	Ile	Thr	Asp	Ile	Ser	Gln	Leu	Lys	Glu	Ala	Ile	Lys	Gln
1				5					10					15	

- 30 -

Tyr His Ser Glu Gly Lys Ser Ile Gly Phe Val Pro Thr Met Gly Phe
 20 25 30
 Leu His Glu Gly His Leu Thr Leu Ala Asp Lys Ala Arg Gln Glu Asn
 35 40 45
 Asp Ala Val Ile Met Ser Ile Phe Val Asn Pro Ala Gln Phe Gly Pro
 50 55 60
 Asn Glu Asp Phe Glu Ala Tyr Pro Arg Asp Ile Glu Arg Asp Ala Ala
 65 70 75 80
 Leu Ala Glu Asn Ala Gly Val Asp Ile Leu Phe Thr Pro Asp Ala His
 85 90 95
 Asp Met Tyr Pro Gly Glu Lys Asn Val Thr Ile His Val Glu Arg Arg
 100 105 110
 Thr Asp Val Leu Cys Gly Arg Ser Arg Glu Gly His Phe Asp Gly Val
 115 120 125
 Ala Ile Val Leu Thr Lys Leu Phe Asn Leu Val Lys Pro Thr Arg Ala
 130 135 140
 Tyr Phe Gly Leu Lys Asp Ala Gln Gln Val Ala Val Val Asp Gly Leu
 145 150 155 160
 Ile Ser Asp Phe Phe Met Asp Ile Glu Leu Val Pro Val Asp Thr Val
 165 170 175
 Arg Glu Glu Asp Gly Leu Ala Lys Ser Ser Arg Asn Val Tyr Leu Thr
 180 185 190
 Ala Glu Glu Arg Lys Glu Ala Pro Lys Leu Tyr Arg Ala Leu Gln Thr
 195 200 205
 Ser Ala Glu Leu Val Gln Ala Gly Glu Arg Asp Pro Glu Ala Val Ile
 210 215 220
 Lys Ala Ala Lys Asp Ile Ile Glu Thr Thr Ser Gly Thr Ile Asp Tyr
 225 230 235 240
 Val Glu Leu Tyr Ser Tyr Pro Glu Leu Glu Pro Val Asn Glu Ile Ala
 245 250 255
 Gly Lys Met Ile Leu Ala Val Ala Val Ala Phe Ser Lys Ala Arg Leu
 260 265 270
 Ile Asp Asn Ile Ile Ile Asp Ile Arg Glu Met Glu Arg Ile
 275 280 285

<210> 27

<211> 381

<212> DNA

<213> Bacillus subtilis

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<220>

<221> CDS

<222> (1)..(381)

<400> 27

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Met	Tyr	Arg	Thr	Met	Met	Ser	Gly	Lys	Leu	His	Arg	Ala	Thr	Val	Thr	
1				5					10					15		
gaa	gca	aac	ctg	aac	tat	gtg	gga	agc	att	aca	att	gat	gaa	gat	ctc	96
Glu	Ala	Asn	Leu	Asn	Tyr	Val	Gly	Ser	Ile	Thr	Ile	Asp	Glu	Asp	Leu	
			20					25					30			
att	gat	gct	gtg	gga	atg	ctt	cct	aat	gaa	aaa	gta	caa	att	gtg	aat	144
Ile	Asp	Ala	Val	Gly	Met	Leu	Pro	Asn	Glu	Lys	Val	Gln	Ile	Val	Asn	
		35					40					45				
aat	aat	aat	gga	gca	cgt	ctt	gaa	acg	tat	att	att	cct	ggt	aaa	cgg	192
Asn	Asn	Asn	Gly	Ala	Arg	Leu	Glu	Thr	Tyr	Ile	Ile	Pro	Gly	Lys	Arg	
	50					55					60					
gga	agc	ggc	gtc	ata	tgc	tta	aac	ggt	gca	gcc	gca	cgc	ctt	gtg	cag	240
Gly	Ser	Gly	Val	Ile	Cys	Leu	Asn	Gly	Ala	Ala	Ala	Arg	Leu	Val	Gln	
65					70					75					80	
gaa	gga	gat	aag	gtc	att	att	att	tcc	tac	aaa	atg	atg	tct	gat	caa	288
Glu	Gly	Asp	Lys	Val	Ile	Ile	Ile	Ser	Tyr	Lys	Met	Met	Ser	Asp	Gln	
				85					90					95		
gaa	gcg	gca	agc	cat	gag	ccg	aaa	gtg	gct	gtt	ctg	aat	gat	caa	aac	336
Glu	Ala	Ala	Ser	His	Glu	Pro	Lys	Val	Ala	Val	Leu	Asn	Asp	Gln	Asn	
			100					105					110			
aaa	att	gaa	caa	atg	ctg	ggg	aac	gaa	cca	gcc	cgt	aca	att	ttg		381
Lys	Ile	Glu	Gln	Met	Leu	Gly	Asn	Glu	Pro	Ala	Arg	Thr	Ile	Leu		
		115					120					125				

<210> 28

<211> 127

<212> PRT

<213> Bacillus subtilis

<400> 28

Met	Tyr	Arg	Thr	Met	Met	Ser	Gly	Lys	Leu	His	Arg	Ala	Thr	Val	Thr
1				5					10					15	
Glu	Ala	Asn	Leu	Asn	Tyr	Val	Gly	Ser	Ile	Thr	Ile	Asp	Glu	Asp	Leu
			20					25					30		
Ile	Asp	Ala	Val	Gly	Met	Leu	Pro	Asn	Glu	Lys	Val	Gln	Ile	Val	Asn
		35					40					45			
Asn	Asn	Asn	Gly	Ala	Arg	Leu	Glu	Thr	Tyr	Ile	Ile	Pro	Gly	Lys	Arg
	50					55					60				
Gly	Ser	Gly	Val	Ile	Cys	Leu	Asn	Gly	Ala	Ala	Ala	Arg	Leu	Val	Gln
65					70					75					80

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Glu Gly Asp Lys Val Ile Ile Ile Ser Tyr Lys Met Met Ser Asp Gln
85 90 95

Glu Ala Ala Ser His Glu Pro Lys Val Ala Val Leu Asn Asp Gln Asn
100 105 110

Lys Ile Glu Gln Met Leu Gly Asn Glu Pro Ala Arg Thr Ile Leu
115 120 125

<210> 29

<211> 894

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> . (1) . . (894)

<400> 29

atg aaa att gga att atc ggc gga ggc tcc gtt ggt ctt tta tgc gcc 48
Met Lys Ile Gly Ile Ile Gly Gly Gly Ser Val Gly Leu Leu Cys Ala
1 5 10 15

tat	tat	ttg	tca	ctt	tat	cac	gac	gtg	act	gtt	gtg	acg	agg	cgg	caa	96
Tyr	Tyr	Leu	Ser	Leu	Tyr	His	Asp	Val	Thr	Val	Val	Thr	Arg	Arg	Gln	
		20						25					30			

gaa cag gct gcg gcc att cag tct gaa gga atc cgg ctt tat aaa ggc 144
Glu Gln Ala Ala Ala Ile Gln Ser Glu Gly Ile Arg Leu Tyr Lys Gly
35 40 45

ggg gag gaa ttc agg gct gat tgc agt gcg gac acg agt atc aat tcg 192
Gly Glu Glu Phe Arg Ala Asp Cys Ser Ala Asp Thr Ser Ile Asn Ser
 50 55 60

gac ttt gac ctg ctt gtc gtg aca gtg aag cag cat cag ctt caa tct 240
Asp Phe Asp Leu Leu Val Val Thr Val Lys Gln His Gln Leu Gln Ser
65 70 75 80

gtt ttt tcg tcg ctt gaa cga atc ggg aag acg aat ata tta ttt ttg 288
Val Phe Ser Ser Leu Glu Arg Ile Gly Lys Thr Asn Ile Leu Phe Leu
85 90 95

caa aac ggc atg ggg cat atc cac gac cta aaa gac tgg cac gtt ggc 336
Gln Asn Gly Met Gly His Ile His Asp Leu Lys Asp Trp His Val Gly
100 105 110

cat tcc att tat gtt gga atc gtt gag cac gga gct gta aga aaa tcg 384
His Ser Ile Tyr Val Gly Ile Val Glu His Gly Ala Val Arg Lys Ser
115 120 125

gat aca gct gtt gat cat aca ggc cta ggt gcg ata aaa tgg agc gcg 432
Asp Thr Ala Val Asp His Thr Gly Leu Gly Ala Ile Lys Trp Ser Ala
130 135 140

ttc gac gat gct qaa cca gac cgg ctg aac atc ttg ttt cag cat aac 480

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Phe 145	Asp	Asp	Ala	Glu	Pro 150	Asp	Arg	Leu	Asn	Ile 155	Leu	Phe	Gln	His	Asn 160	
cat	tcg	gat	ttt	ccg	att	tat	tat	gag	acg	gat	tgg	tac	cgt	ctg	ctg	528
His	Ser	Asp	Phe	Pro 165	Ile	Tyr	Tyr	Glu	Thr 170	Asp	Trp	Tyr	Arg	Leu 175	Leu	
acg	ggc	aag	ctg	att	gta	aat	gcg	tgt	att	aat	cct	tta	act	gcg	tta	576
Thr	Gly	Lys	Leu 180	Ile	Val	Asn	Ala	Cys 185	Ile	Asn	Pro	Leu	Thr 190	Ala	Leu	
ttg	caa	gtg	aaa	aat	gga	gaa	ctg	ctg	aca	acg	cca	gct	tat	ctg	gct	624
Leu	Gln	Val 195	Lys	Asn	Gly	Glu	Leu 200	Leu	Thr	Thr	Pro	Ala 205	Tyr	Leu	Ala	
ttt	atg	aag	ctg	gta	ttt	cag	gag	gca	tgc	cgc	att	tta	aaa	ctt	gaa	672
Phe	Met 210	Lys	Leu	Val	Phe	Gln 215	Glu	Ala	Cys	Arg	Ile 220	Leu	Lys	Leu	Glu	
aat	gaa	gaa	aag	gct	tgg	gag	cgg	gtt	cag	gcc	gtt	tgt	ggg	caa	acg	720
Asn 225	Glu	Glu	Lys	Ala	Trp 230	Glu	Arg	Val	Gln	Ala 235	Val	Cys	Gly	Gln	Thr 240	
aaa	gag	aat	cgt	tca	tca	atg	ctg	gtt	gac	gtc	att	gga	ggc	cgg	cag	768
Lys	Glu	Asn	Arg	Ser 245	Ser	Met	Leu	Val	Asp 250	Val	Ile	Gly	Gly	Arg 255	Gln	
acg	gaa	gct	gac	gcc	att	atc	gga	tac	tta	ttg	aag	gaa	gca	agt	ctt	816
Thr	Glu	Ala	Asp 260	Ala	Ile	Ile	Gly	Tyr 265	Leu	Leu	Lys	Glu	Ala 270	Ser	Leu	
caa	ggt	ctt	gat	gcc	gtc	cac	cta	gag	ttt	tta	tat	ggc	agc	atc	aaa	864
Gln	Gly	Leu 275	Asp	Ala	Val	His	Leu 280	Glu	Phe	Leu	Tyr	Gly 285	Ser	Ile	Lys	
gca	ttg	gag	cga	aat	aca	aac	aaa	gtc	ttt							894
Ala 290	Leu	Glu	Arg	Asn	Thr	Asn 295	Lys	Val	Phe							

<210> 30

<211> 298

<212> PRT

<213> Bacillus subtilis

<400> 30

Met	Lys	Ile	Gly	Ile	Ile	Gly	Gly	Gly	Ser	Val	Gly	Leu	Leu	Cys	Ala
1				5					10					15	

Tyr	Tyr	Leu	Ser	Leu	Tyr	His	Asp	Val	Thr	Val	Val	Thr	Arg	Arg	Gln
			20					25					30		

Glu	Gln	Ala	Ala	Ala	Ile	Gln	Ser	Glu	Gly	Ile	Arg	Leu	Tyr	Lys	Gly
		35					40					45			

Gly	Glu	Glu	Phe	Arg	Ala	Asp	Cys	Ser	Ala	Asp	Thr	Ser	Ile	Asn	Ser
	50					55					60				

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Asp Phe Asp Leu Leu Val Val Thr Val Lys Gln His Gln Leu Gln Ser
 65 70 75 80
 Val Phe Ser Ser Leu Glu Arg Ile Gly Lys Thr Asn Ile Leu Phe Leu
 85 90 95
 Gln Asn Gly Met Gly His Ile His Asp Leu Lys Asp Trp His Val Gly
 100 105 110
 His Ser Ile Tyr Val Gly Ile Val Glu His Gly Ala Val Arg Lys Ser
 115 120 125
 Asp Thr Ala Val Asp His Thr Gly Leu Gly Ala Ile Lys Trp Ser Ala
 130 135 140
 Phe Asp Asp Ala Glu Pro Asp Arg Leu Asn Ile Leu Phe Gln His Asn
 145 150 155 160
 His Ser Asp Phe Pro Ile Tyr Tyr Glu Thr Asp Trp Tyr Arg Leu Leu
 165 170 175
 Thr Gly Lys Leu Ile Val Asn Ala Cys Ile Asn Pro Leu Thr Ala Leu
 180 185 190
 Leu Gln Val Lys Asn Gly Glu Leu Leu Thr Thr Pro Ala Tyr Leu Ala
 195 200 205
 Phe Met Lys Leu Val Phe Gln Glu Ala Cys Arg Ile Leu Lys Leu Glu
 210 215 220
 Asn Glu Glu Lys Ala Trp Glu Arg Val Gln Ala Val Cys Gly Gln Thr
 225 230 235 240
 Lys Glu Asn Arg Ser Ser Met Leu Val Asp Val Ile Gly Gly Arg Gln
 245 250 255
 Thr Glu Ala Asp Ala Ile Ile Gly Tyr Leu Leu Lys Glu Ala Ser Leu
 260 265 270
 Gln Gly Leu Asp Ala Val His Leu Glu Phe Leu Tyr Gly Ser Ile Lys
 275 280 285
 Ala Leu Glu Arg Asn Thr Asn Lys Val Phe
 290 295

<210> 31

<211> 1725

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(1722)

<400> 31

atg ggg act aat gta cag gtg gat tca gca tct gcc gaa tgt aca cag 48
 Met Gly Thr Asn Val Gln Val Asp Ser Ala Ser Ala Glu Cys Thr Gln

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1				5					10					15		
acg	atg	agc	gga	gca	tta	atg	ctg	att	gaa	tca	tta	aaa	aaa	gag	aaa	96
Thr	Met	Ser	Gly	Ala	Leu	Met	Leu	Ile	Glu	Ser	Leu	Lys	Lys	Glu	Lys	
			20					25					30			
gta	gaa	atg	atc	ttc	ggt	tat	ccg	ggc	ggg	gct	gtg	ctt	ccg	att	tac	144
Val	Glu	Met	Ile	Phe	Gly	Tyr	Pro	Gly	Gly	Ala	Val	Leu	Pro	Ile	Tyr	
		35					40					45				
gat	aag	cta	tac	aat	tca	ggg	ttg	gta	cat	atc	ctt	ccc	cgt	cac	gaa	192
Asp	Lys	Leu	Tyr	Asn	Ser	Gly	Leu	Val	His	Ile	Leu	Pro	Arg	His	Glu	
	50					55					60					
caa	gga	gca	att	cat	gca	gcg	gag	gga	tac	gca	agg	gtc	tcc	gga	aaa	240
Gln	Gly	Ala	Ile	His	Ala	Ala	Glu	Gly	Tyr	Ala	Arg	Val	Ser	Gly	Lys	
	65				70				75						80	
ccg	ggt	gtc	gtc	att	gcc	acg	tca	ggg	ccg	gga	gcg	aca	aac	ctt	ggt	288
Pro	Gly	Val	Val	Ile	Ala	Thr	Ser	Gly	Pro	Gly	Ala	Thr	Asn	Leu	Val	
				85				90						95		
aca	ggc	ctt	gct	gat	gcc	atg	att	gat	tca	ttg	ccg	tta	gtc	gtc	ttt	336
Thr	Gly	Leu	Ala	Asp	Ala	Met	Ile	Asp	Ser	Leu	Pro	Leu	Val	Val	Phe	
			100					105					110			
aca	ggg	cag	gta	gca	acc	tct	gta	atc	ggg	agc	gat	gca	ttt	cag	gaa	384
Thr	Gly	Gln	Val	Ala	Thr	Ser	Val	Ile	Gly	Ser	Asp	Ala	Phe	Gln	Glu	
		115					120					125				
gca	gac	att	tta	ggg	att	acg	atg	cca	gta	aca	aaa	cac	agc	tac	cag	432
Ala	Asp	Ile	Leu	Gly	Ile	Thr	Met	Pro	Val	Thr	Lys	His	Ser	Tyr	Gln	
	130					135					140					
gtt	cgc	cag	ccg	gaa	gat	ctg	ccg	cgc	atc	att	aaa	gaa	gcg	ttc	cat	480
Val	Arg	Gln	Pro	Glu	Asp	Leu	Pro	Arg	Ile	Ile	Lys	Glu	Ala	Phe	His	
	145				150					155					160	
att	gca	aca	act	gga	aga	ccc	gga	cct	gta	ttg	att	gat	att	ccg	aaa	528
Ile	Ala	Thr	Thr	Gly	Arg	Pro	Gly	Pro	Val	Leu	Ile	Asp	Ile	Pro	Lys	
				165				170						175		
gat	gta	gca	aca	att	gaa	gga	gaa	ttc	agc	tac	gat	cat	gag	atg	aat	576
Asp	Val	Ala	Thr	Ile	Glu	Gly	Glu	Phe	Ser	Tyr	Asp	His	Glu	Met	Asn	
			180					185					190			
ctc	ccg	gga	tac	cag	ccg	aca	aca	gag	ccg	aat	tat	ttg	cag	atc	cgc	624
Leu	Pro	Gly	Tyr	Gln	Pro	Thr	Thr	Glu	Pro	Asn	Tyr	Leu	Gln	Ile	Arg	
		195					200					205				
aag	ctt	gtg	gaa	gcc	gtg	agc	agt	gcg	aaa	aaa	ccg	gtg	atc	ctg	gcg	672
Lys	Leu	Val	Glu	Ala	Val	Ser	Ser	Ala	Lys	Lys	Pro	Val	Ile	Leu	Ala	
	210					215					220					
ggt	gcg	ggc	gta	ctg	cac	gga	aaa	gcg	tca	gaa	gaa	tta	aaa	aat	tat	720
Gly	Ala	Gly	Val	Leu	His	Gly	Lys	Ala	Ser	Glu	Glu	Leu	Lys	Asn	Tyr	
	225				230					235					240	

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gct gaa cag cag caa atc cct gtg gca cac acc ctt ttg ggg ctc gga	768
Ala Glu Gln Gln Gln Ile Pro Val Ala His Thr Leu Leu Gly Leu Gly	
245 250 255	
ggc ttc ccg gct gac cat ccg ctt ttc cta ggg atg gcg gga atg cac	816
Gly Phe Pro Ala Asp His Pro Leu Phe Leu Gly Met Ala Gly Met His	
260 265 270	
ggt act tat aca gcc aat atg gcc ctt cat gaa tgt gat cta tta atc	864
Gly Thr Tyr Thr Ala Asn Met Ala Leu His Glu Cys Asp Leu Leu Ile	
275 280 285	
agt atc ggc gcc cgt ttt gat gac cgt gtc aca gga aac ctg aaa cac	912
Ser Ile Gly Ala Arg Phe Asp Arg Val Thr Gly Asn Leu Lys His	
290 295 300	
ttt gcc aga aac gca aag ata gcc cac atc gat att gat cca gct gaa	960
Phe Ala Arg Asn Ala Lys Ile Ala His Ile Asp Ile Asp Pro Ala Glu	
305 310 315 320	
atc gga aaa atc atg aaa aca cag att cct gta gtc gga gac agc aaa	1008
Ile Gly Lys Ile Met Lys Thr Gln Ile Pro Val Val Gly Asp Ser Lys	
325 330 335	
att gtc ctg cag gag ctg atc aaa caa gac ggc aaa caa agc gat tca	1056
Ile Val Leu Gln Glu Leu Ile Lys Gln Asp Gly Lys Gln Ser Asp Ser	
340 345 350	
agc gaa tgg aaa aaa cag ctc gca gaa tgg aaa gaa gag tat ccg ctc	1104
Ser Glu Trp Lys Lys Gln Leu Ala Glu Trp Lys Glu Glu Tyr Pro Leu	
355 360 365	
tgg tat gta gat aat gaa gaa gaa ggt ttt aaa cct cag aaa ttg att	1152
Trp Tyr Val Asp Asn Glu Glu Glu Gly Phe Lys Pro Gln Lys Leu Ile	
370 375 380	
gaa tat att cat caa ttt aca aaa gga gag gcc att gtc gca acg gat	1200
Glu Tyr Ile His Gln Phe Thr Lys Gly Glu Ala Ile Val Ala Thr Asp	
385 390 395 400	
gta ggc cag cat caa atg tgg tca gcg caa ttt tat ccg ttc caa aaa	1248
Val Gly Gln His Gln Met Trp Ser Ala Gln Phe Tyr Pro Phe Gln Lys	
405 410 415	
gca gat aaa tgg gtc acg tca gcc gga ctt gga acg atg gga ttc ggt	1296
Ala Asp Lys Trp Val Thr Ser Gly Gly Leu Gly Thr Met Gly Phe Gly	
420 425 430	
ctt ccg gcg gcg atc ggc gca cag ctg gcc gaa aaa gat gct act gtt	1344
Leu Pro Ala Ala Ile Gly Ala Gln Leu Ala Glu Lys Asp Ala Thr Val	
435 440 445	
gtc gcg gtt gtc gga gac ggc gga ttc caa atg acg ctt caa gaa ctc	1392
Val Ala Val Val Gly Asp Gly Gly Phe Gln Met Thr Leu Gln Glu Leu	
450 455 460	
gat gtt att cgc gaa tta aat ctt ccg gtc aag gta gtg att tta aat	1440
Asp Val Ile Arg Glu Leu Asn Leu Pro Val Lys Val Val Ile Leu Asn	

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465	470	475	480	
aac gct tgt ctc gga atg gtc aga cag tgg cag gaa att ttc tat gaa				1488
Asn Ala Cys Leu Gly Met Val Arg Gln Trp Gln Glu Ile Phe Tyr Glu				
	485	490	495	
gaa cgt tat tca gaa tct aaa ttc gct tct cag cct gac ttc gtc aaa				1536
Glu Arg Tyr Ser Glu Ser Lys Phe Ala Ser Gln Pro Asp Phe Val Lys				
	500	505	510	
ttg tcc gaa gca tac ggc att aaa ggc atc aga att tca tca gaa gcg				1584
Leu Ser Glu Ala Tyr Gly Ile Lys Gly Ile Arg Ile Ser Ser Glu Ala				
	515	520	525	
gaa gca aag gaa aag ctg gaa gag gca tta aca tca aga gaa cct gtt				1632
Glu Ala Lys Glu Lys Leu Glu Glu Ala Leu Thr Ser Arg Glu Pro Val				
	530	535	540	
gtc att gac gtg cgg gtt gcc agc gaa gaa aaa gta ttc ccg atg gtg				1680
Val Ile Asp Val Arg Val Ala Ser Glu Glu Lys Val Phe Pro Met Val				
	545	550	555	560
gct ccg ggg aaa ggg ctg cat gaa atg gtg ggg gtg aaa cct tga				1725
Ala Pro Gly Lys Gly Leu His Glu Met Val Gly Val Lys Pro				
	565	570		

<210> 32

<211> 574

<212> PRT

<213> Bacillus subtilis

<400> 32

Met Gly Thr Asn Val Gln Val Asp Ser Ala Ser Ala Glu Cys Thr Gln
1 5 10 15

Thr Met Ser Gly Ala Leu Met Leu Ile Glu Ser Leu Lys Lys Glu Lys
20 25 30

Val Glu Met Ile Phe Gly Tyr Pro Gly Gly Ala Val Leu Pro Ile Tyr
35 40 45

Asp Lys Leu Tyr Asn Ser Gly Leu Val His Ile Leu Pro Arg His Glu
50 55 60

Gln Gly Ala Ile His Ala Ala Glu Gly Tyr Ala Arg Val Ser Gly Lys
65 70 75 80

Pro Gly Val Val Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
85 90 95

Thr Gly Leu Ala Asp Ala Met Ile Asp Ser Leu Pro Leu Val Val Phe
100 105 110

Thr Gly Gln Val Ala Thr Ser Val Ile Gly Ser Asp Ala Phe Gln Glu
115 120 125

Ala Asp Ile Leu Gly Ile Thr Met Pro Val Thr Lys His Ser Tyr Gln

130	135	140														
Val 145	Arg	Gln	Pro	Glu	Asp 150	Leu	Pro	Arg	Ile	Ile 155	Lys	Glu	Ala	Phe	His 160	
Ile	Ala	Thr	Thr	Gly 165	Arg	Pro	Gly	Pro	Val 170	Leu	Ile	Asp	Ile	Pro	Lys 175	
Asp	Val	Ala	Thr 180	Ile	Glu	Gly	Glu	Phe 185	Ser	Tyr	Asp	His	Glu 190	Met	Asn	
Leu	Pro	Gly 195	Tyr	Gln	Pro	Thr	Thr 200	Glu	Pro	Asn	Tyr	Leu 205	Gln	Ile	Arg	
Lys 210	Leu	Val	Glu	Ala	Val	Ser 215	Ser	Ala	Lys	Lys	Pro 220	Val	Ile	Leu	Ala	
Gly 225	Ala	Gly	Val	Leu	His 230	Gly	Lys	Ala	Ser	Glu 235	Glu	Leu	Lys	Asn	Tyr 240	
Ala	Glu	Gln	Gln	Gln 245	Ile	Pro	Val	Ala	His 250	Thr	Leu	Leu	Gly	Leu 255	Gly	
Gly	Phe	Pro	Ala 260	Asp	His	Pro	Leu	Phe 265	Leu	Gly	Met	Ala	Gly 270	Met	His	
Gly	Thr	Tyr	Thr 275	Ala	Asn	Met	Ala 280	Leu	His	Glu	Cys	Asp 285	Leu	Leu	Ile	
Ser	Ile	Gly	Ala	Arg	Phe	Asp 295	Asp	Arg	Val	Thr	Gly 300	Asn	Leu	Lys	His	
Phe 305	Ala	Arg	Asn	Ala	Lys 310	Ile	Ala	His	Ile	Asp 315	Ile	Asp	Pro	Ala	Glu 320	
Ile	Gly	Lys	Ile	Met 325	Lys	Thr	Gln	Ile	Pro 330	Val	Val	Gly	Asp	Ser 335	Lys	
Ile	Val	Leu	Gln 340	Glu	Leu	Ile	Lys	Gln 345	Asp	Gly	Lys	Gln	Ser 350	Asp	Ser	
Ser	Glu	Trp 355	Lys	Lys	Gln	Leu	Ala 360	Glu	Trp	Lys	Glu	Glu 365	Tyr	Pro	Leu	
Trp 370	Tyr	Val	Asp	Asn	Glu	Glu 375	Glu	Gly	Phe	Lys	Pro 380	Gln	Lys	Leu	Ile	
Glu 385	Tyr	Ile	His	Gln	Phe 390	Thr	Lys	Gly	Glu	Ala 395	Ile	Val	Ala	Thr	Asp 400	
Val	Gly	Gln	His 405	Gln	Met	Trp	Ser	Ala	Gln 410	Phe	Tyr	Pro	Phe	Gln 415	Lys	
Ala	Asp	Lys	Trp 420	Val	Thr	Ser	Gly	Gly 425	Leu	Gly	Thr	Met	Gly 430	Phe	Gly	
Leu	Pro	Ala	Ala	Ile	Gly	Ala 440	Gln	Leu	Ala	Glu	Lys	Asp 445	Ala	Thr	Val	

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Val	Ala	Val	Val	Gly	Asp	Gly	Gly	Phe	Gln	Met	Thr	Leu	Gln	Glu	Leu
450						455					460				
Asp	Val	Ile	Arg	Glu	Leu	Asn	Leu	Pro	Val	Lys	Val	Val	Ile	Leu	Asn
465					470					475					480
Asn	Ala	Cys	Leu	Gly	Met	Val	Arg	Gln	Trp	Gln	Glu	Ile	Phe	Tyr	Glu
				485					490					495	
Glu	Arg	Tyr	Ser	Glu	Ser	Lys	Phe	Ala	Ser	Gln	Pro	Asp	Phe	Val	Lys
			500					505					510		
Leu	Ser	Glu	Ala	Tyr	Gly	Ile	Lys	Gly	Ile	Arg	Ile	Ser	Ser	Glu	Ala
		515					520					525			
Glu	Ala	Lys	Glu	Lys	Leu	Glu	Glu	Ala	Leu	Thr	Ser	Arg	Glu	Pro	Val
	530					535					540				
Val	Ile	Asp	Val	Arg	Val	Ala	Ser	Glu	Glu	Lys	Val	Phe	Pro	Met	Val
545					550					555					560
Ala	Pro	Gly	Lys	Gly	Leu	His	Glu	Met	Val	Gly	Val	Lys	Pro		
				565					570						

<210> 33

<211> 525

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(522)

<400> 33

ttg	aaa	aga	att	atc	aca	ttg	act	gtg	gtg	aac	cgc	tcc	ggg	gtg	tta	48
Met	Lys	Arg	Ile	Ile	Thr	Leu	Thr	Val	Val	Asn	Arg	Ser	Gly	Val	Leu	
1				5				10					15			
aac	cgg	atc	acc	ggt	cta	ttc	aca	aaa	agg	cat	tac	aac	att	gaa	agc	96
Asn	Arg	Ile	Thr	Gly	Leu	Phe	Thr	Lys	Arg	His	Tyr	Asn	Ile	Glu	Ser	
			20					25					30			
att	aca	gtt	gga	cac	aca	gaa	aca	gcc	ggc	gtt	tcc	aga	atc	acc	ttc	144
Ile	Thr	Val	Gly	His	Thr	Glu	Thr	Ala	Gly	Val	Ser	Arg	Ile	Thr	Phe	
		35				40					45					
gtc	gtt	cat	gtt	gaa	ggt	gaa	aat	gat	gtt	gaa	cag	tta	acg	aaa	cag	192
Val	Val	His	Val	Glu	Gly	Glu	Asn	Asp	Val	Glu	Gln	Leu	Thr	Lys	Gln	
	50				55						60					
ctc	aac	aaa	cag	att	gat	gtg	ctg	aaa	gtc	aca	gac	atc	aca	aat	caa	240
Leu	Asn	Lys	Gln	Ile	Asp	Val	Leu	Lys	Val	Thr	Asp	Ile	Thr	Asn	Gln	
65					70				75						80	
tcg	att	gtc	cag	agg	gag	ctg	gcc	tta	atc	aag	gtt	gtc	tcc	gca	cct	288
Ser	Ile	Val	Gln	Arg	Glu	Leu	Ala	Leu	Ile	Lys	Val	Val	Ser	Ala	Pro	

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85								90					95				
tca	aca	aga	aca	gag	att	aat	gga	atc	ata	gaa	ccg	ttt	aga	gcc	tct	336	
Ser	Thr	Arg	Thr	Glu	Ile	Asn	Gly	Ile	Ile	Glu	Pro	Phe	Arg	Ala	Ser		
			100					105					110				
gtc	gtt	gat	gtc	agc	aga	gac	agc	atc	gtt	gtt	cag	gtg	aca	ggg	gaa	384	
Val	Val	Asp	Val	Ser	Arg	Asp	Ser	Ile	Val	Val	Gln	Val	Thr	Gly	Glu		
		115					120					125					
tct	aac	aaa	att	gaa	gcg	ctt	att	gag	tta	tta	aaa	cct	tat	ggc	att	432	
Ser	Asn	Lys	Ile	Glu	Ala	Leu	Ile	Glu	Leu	Leu	Lys	Pro	Tyr	Gly	Ile		
	130					135					140						
aaa	gaa	atc	gcg	aga	aca	ggg	aca	acg	gct	ttt	gcg	agg	gga	acc	agc	480	
Lys	Glu	Ile	Ala	Arg	Thr	Gly	Thr	Thr	Ala	Phe	Ala	Arg	Gly	Thr	Ser		
145					150					155					160		
aaa	agg	cgt	cat	cca	ata	aaa	caa	tat	cta	ttg	tat	aaa	aca	taa		525	
Lys	Arg	Arg	His	Pro	Ile	Lys	Gln	Tyr	Leu	Leu	Tyr	Lys	Thr				
				165					170								

<210> 34

<211> 174

<212> PRT

<213> Bacillus subtilis

<400> 34

Met	Lys	Arg	Ile	Ile	Thr	Leu	Thr	Val	Val	Asn	Arg	Ser	Gly	Val	Leu
1				5					10					15	

Asn	Arg	Ile	Thr	Gly	Leu	Phe	Thr	Lys	Arg	His	Tyr	Asn	Ile	Glu	Ser
			20					25					30		

Ile	Thr	Val	Gly	His	Thr	Glu	Thr	Ala	Gly	Val	Ser	Arg	Ile	Thr	Phe
		35					40					45			

Val	Val	His	Val	Glu	Gly	Glu	Asn	Asp	Val	Glu	Gln	Leu	Thr	Lys	Gln
	50					55					60				

Leu	Asn	Lys	Gln	Ile	Asp	Val	Leu	Lys	Val	Thr	Asp	Ile	Thr	Asn	Gln
65					70					75					80

Ser	Ile	Val	Gln	Arg	Glu	Leu	Ala	Leu	Ile	Lys	Val	Val	Ser	Ala	Pro
				85					90					95	

Ser	Thr	Arg	Thr	Glu	Ile	Asn	Gly	Ile	Ile	Glu	Pro	Phe	Arg	Ala	Ser
			100					105					110		

Val	Val	Asp	Val	Ser	Arg	Asp	Ser	Ile	Val	Val	Gln	Val	Thr	Gly	Glu
		115					120					125			

Ser	Asn	Lys	Ile	Glu	Ala	Leu	Ile	Glu	Leu	Leu	Lys	Pro	Tyr	Gly	Ile
	130					135					140				

Lys	Glu	Ile	Ala	Arg	Thr	Gly	Thr	Thr	Ala	Phe	Ala	Arg	Gly	Thr	Ser
145					150					155					160

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Lys Arg Arg His Pro Ile Lys Gln Tyr Leu Leu Tyr Lys Thr
 165 170

<210> 35

<211> 1029

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(1026)

<400> 35

atg gta aaa gta tat tat aac ggt gat atc aaa gag aac gta ttg gct 48
 Met Val Lys Val Tyr Tyr Asn Gly Asp Ile Lys Glu Asn Val Leu Ala
 1 5 10 15

gga aaa aca gta gcg gtt atc ggg tac ggt tcg caa ggc cac gca cat 96
 Gly Lys Thr Val Ala Val Ile Gly Tyr Gly Ser Gln Gly His Ala His
 20 25 30

gcc ctg aac ctt aaa gaa agc gga gta gac gtg atc gtc ggt gtt aga 144
 Ala Leu Asn Leu Lys Glu Ser Gly Val Asp Val Ile Val Gly Val Arg
 35 40 45

caa gga aaa tct ttc act caa gcc caa gaa gac gga cat aaa gta ttt 192
 Gln Gly Lys Ser Phe Thr Gln Ala Gln Glu Asp Gly His Lys Val Phe
 50 55 60

tca gta aaa gaa gcg gca gcc caa gcc gaa atc atc atg gtt ctg ctt 240
 Ser Val Lys Glu Ala Ala Ala Gln Ala Glu Ile Ile Met Val Leu Leu
 65 70 75 80

ccg gat gag cag cag caa aaa gta tac gaa gct gaa atc aaa gat gaa 288
 Pro Asp Glu Gln Gln Gln Lys Val Tyr Glu Ala Glu Ile Lys Asp Glu
 85 90 95

ttg aca gca gga aaa tca tta gta ttc gct cat gga ttt aac gtg cat 336
 Leu Thr Ala Gly Lys Ser Leu Val Phe Ala His Gly Phe Asn Val His
 100 105 110

ttc cat caa att gtt cct ccg gcg gat gta gat gta ttc tta gtg gcc 384
 Phe His Gln Ile Val Pro Pro Ala Asp Val Asp Val Phe Leu Val Ala
 115 120 125

cct aaa ggc ccg gga cac ttg gta aga aga aca tat gag caa gga gct 432
 Pro Lys Gly Pro Gly His Leu Val Arg Arg Thr Tyr Glu Gln Gly Ala
 130 135 140

ggc gta cct gca ttg ttc gca atc tat caa gat gtg act gga gaa gca 480
 Gly Val Pro Ala Leu Phe Ala Ile Tyr Gln Asp Val Thr Gly Glu Ala
 145 150 155 160

aga gac aaa gcc ctc gct tat gct aaa gga atc ggc ggc gca aga gcg 528
 Arg Asp Lys Ala Leu Ala Tyr Ala Lys Gly Ile Gly Gly Ala Arg Ala
 165 170 175

- 42 -

ggc gta tta gaa acg aca ttt aaa gaa gaa aca gaa aca gat ttg ttc 576
 Gly Val Leu Glu Thr Thr Phe Lys Glu Glu Thr Glu Thr Asp Leu Phe
 180 185 190

ggt gag caa gca gtt ctt tgc ggc gga tta agc gcg ctt gtc aaa gcc 624
 Gly Glu Gln Ala Val Leu Cys Gly Gly Leu Ser Ala Leu Val Lys Ala
 195 200 205

gga ttt gaa acc tta act gaa gca ggt tat cag cct gaa ctt gca tac 672
 Gly Phe Glu Thr Leu Thr Glu Ala Gly Tyr Gln Pro Glu Leu Ala Tyr
 210 215 220

ttc gag tgt ctt cat gag ctg aaa tta atc gta gac ctt atg tac gaa 720
 Phe Glu Cys Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Tyr Glu
 225 230 235 240

gaa gga ctt gca gga atg aga tat tca atc tct gac aca gca cag tgg 768
 Glu Gly Leu Ala Gly Met Arg Tyr Ser Ile Ser Asp Thr Ala Gln Trp
 245 250 255

gga gat ttc gta tca ggc cct cgc gtt gtg gac gcc aaa gta aaa gaa 816
 Gly Asp Phe Val Ser Gly Pro Arg Val Val Asp Ala Lys Val Lys Glu
 260 265 270

tct atg aaa gaa gta tta aaa gat atc caa aac ggt aca ttc gca aaa 864
 Ser Met Lys Glu Val Leu Lys Asp Ile Gln Asn Gly Thr Phe Ala Lys
 275 280 285

gag tgg atc gtc gaa aac caa gta aac cgt cct cgt ttc aac gct atc 912
 Glu Trp Ile Val Glu Asn Gln Val Asn Arg Pro Arg Phe Asn Ala Ile
 290 295 300

aat gca agc gag aac gaa cat caa atc gaa gta gtg gga aga aag ctt 960
 Asn Ala Ser Glu Asn Glu His Gln Ile Glu Val Val Gly Arg Lys Leu
 305 310 315 320

cgt gaa atg atg ccg ttt gtg aaa caa ggc aag aag aag gaa gcg gtg 1008
 Arg Glu Met Met Pro Phe Val Lys Gln Gly Lys Lys Lys Glu Ala Val
 325 330 335

gtc tcc gtt gcg caa aat taa 1029
 Val Ser Val Ala Gln Asn
 340

<210> 36

<211> 342

<212> PRT

<213> Bacillus subtilis

<400> 36

Met Val Lys Val Tyr Tyr Asn Gly Asp Ile Lys Glu Asn Val Leu Ala
 1 5 10 15

Gly Lys Thr Val Ala Val Ile Gly Tyr Gly Ser Gln Gly His Ala His
 20 25 30

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Ala	Leu	Asn	Leu	Lys	Glu	Ser	Gly	Val	Asp	Val	Ile	Val	Gly	Val	Arg			
		35					40					45						
Gln	Gly	Lys	Ser	Phe	Thr	Gln	Ala	Gln	Glu	Asp	Gly	His	Lys	Val	Phe			
	50					55					60							
Ser	Val	Lys	Glu	Ala	Ala	Ala	Gln	Ala	Glu	Ile	Ile	Met	Val	Leu	Leu			
65					70					75					80			
Pro	Asp	Glu	Gln	Gln	Gln	Lys	Val	Tyr	Glu	Ala	Glu	Ile	Lys	Asp	Glu			
				85					90					95				
Leu	Thr	Ala	Gly	Lys	Ser	Leu	Val	Phe	Ala	His	Gly	Phe	Asn	Val	His			
			100					105					110					
Phe	His	Gln	Ile	Val	Pro	Pro	Ala	Asp	Val	Asp	Val	Phe	Leu	Val	Ala			
		115					120					125						
Pro	Lys	Gly	Pro	Gly	His	Leu	Val	Arg	Arg	Thr	Tyr	Glu	Gln	Gly	Ala			
	130					135					140							
Gly	Val	Pro	Ala	Leu	Phe	Ala	Ile	Tyr	Gln	Asp	Val	Thr	Gly	Glu	Ala			
145					150					155					160			
Arg	Asp	Lys	Ala	Leu	Ala	Tyr	Ala	Lys	Gly	Ile	Gly	Gly	Ala	Arg	Ala			
				165					170					175				
Gly	Val	Leu	Glu	Thr	Thr	Phe	Lys	Glu	Glu	Thr	Glu	Thr	Asp	Leu	Phe			
			180					185					190					
Gly	Glu	Gln	Ala	Val	Leu	Cys	Gly	Gly	Leu	Ser	Ala	Leu	Val	Lys	Ala			
		195					200					205						
Gly	Phe	Glu	Thr	Leu	Thr	Glu	Ala	Gly	Tyr	Gln	Pro	Glu	Leu	Ala	Tyr			
	210					215					220							
Phe	Glu	Cys	Leu	His	Glu	Leu	Lys	Leu	Ile	Val	Asp	Leu	Met	Tyr	Glu			
225					230					235					240			
Glu	Gly	Leu	Ala	Gly	Met	Arg	Tyr	Ser	Ile	Ser	Asp	Thr	Ala	Gln	Trp			
				245					250					255				
Gly	Asp	Phe	Val	Ser	Gly	Pro	Arg	Val	Val	Asp	Ala	Lys	Val	Lys	Glu			
			260					265					270					
Ser	Met	Lys	Glu	Val	Leu	Lys	Asp	Ile	Gln	Asn	Gly	Thr	Phe	Ala	Lys			
		275					280					285						
Glu	Trp	Ile	Val	Glu	Asn	Gln	Val	Asn	Arg	Pro	Arg	Phe	Asn	Ala	Ile			
	290					295					300							
Asn	Ala	Ser	Glu	Asn	Glu	His	Gln	Ile	Glu	Val	Val	Gly	Arg	Lys	Leu			
305					310					315					320			
Arg	Glu	Met	Met	Pro	Phe	Val	Lys	Gln	Gly	Lys	Lys	Lys	Glu	Ala	Val			
				325					330					335				
Val	Ser	Val	Ala	Gln	Asn													

340

<210> 37
 <211> 1674
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(1674)

<400> 37

atg gca gaa tta cgc agt aat	atg atc aca caa gga atc gat aga gct	48
Met Ala Glu Leu Arg Ser Asn	Met Ile Thr Gln Gly Ile Asp Arg Ala	
1 5	10 15	
ccg cac cgc agt ttg ctt cgt	gca gca ggg gta aaa gaa gag gat ttc	96
Pro His Arg Ser Leu Leu Arg	Ala Ala Gly Val Lys Glu Glu Asp Phe	
20 25	30	
ggc aag ccg ttt att gcg gtg	tgt aat tca tac att gat atc gtt ccc	144
Gly Lys Pro Phe Ile Ala Val	Cys Asn Ser Tyr Ile Asp Ile Val Pro	
35 40	45	
ggc cat gtt cac ttg cag gag	ttt ggg aaa atc gta aaa gaa gca atc	192
Gly His Val His Leu Gln Glu	Phe Gly Lys Ile Val Lys Glu Ala Ile	
50 55	60	
aga gaa gca ggg ggc gtt ccg	ttt gaa ttt aat acc att ggg gta gat	240
Arg Glu Ala Gly Gly Val Pro	Phe Glu Phe Asn Thr Ile Gly Val Asp	
65 70	75 80	
gat ggc atc gca atg ggg cat	atc ggt atg aga tat tgc ctg cca agc	288
Asp Gly Ile Ala Met Gly His	Ile Gly Met Arg Tyr Ser Leu Pro Ser	
85 90	95	
cgt gaa att atc gca gac tct	gtg gaa acg gtt gta tcc gca cac tgg	336
Arg Glu Ile Ile Ala Asp Ser	Val Glu Thr Val Val Ser Ala His Trp	
100 105	110	
ttt gac gga atg gtc tgt att	ccg aac tgc gac aaa atc aca ccg gga	384
Phe Asp Gly Met Val Cys Ile	Pro Asn Cys Asp Lys Ile Thr Pro Gly	
115 120	125	
atg ctt atg gcg gca atg cgc	atc aac att ccg acg att ttt gtc agc	432
Met Leu Met Ala Ala Met Arg	Ile Asn Ile Pro Thr Ile Phe Val Ser	
130 135	140	
ggc gga ccg atg gcg gca gga	aga aca agt tac ggg cga aaa atc tcc	480
Gly Gly Pro Met Ala Ala Gly	Arg Thr Ser Tyr Gly Arg Lys Ile Ser	
145 150	155 160	
ctt tcc tca gta ttc gaa ggg	gta ggc gcc tac caa gca ggg aaa atc	528
Leu Ser Ser Val Phe Glu Gly	Val Gly Ala Tyr Gln Ala Gly Lys Ile	
165 170	175	
aac gaa aac gag ctt caa gaa	cta gag cag ttc gga tgc cca acg tgc	576

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Asn	Glu	Asn	Glu	Leu	Gln	Glu	Leu	Glu	Gln	Phe	Gly	Cys	Pro	Thr	Cys	
			180					185					190			
ggg	tct	tgc	tca	ggc	atg	ttt	acg	gcg	aac	tca	atg	aac	tgt	ctg	tca	624
Gly	Ser	Cys	Ser	Gly	Met	Phe	Thr	Ala	Asn	Ser	Met	Asn	Cys	Leu	Ser	
		195					200					205				
gaa	gca	ctt	ggt	ctt	gct	ttg	ccg	ggt	aat	gga	acc	att	ctg	gca	aca	672
Glu	Ala	Leu	Gly	Leu	Ala	Leu	Pro	Gly	Asn	Gly	Thr	Ile	Leu	Ala	Thr	
	210					215					220					
tct	ccg	gaa	cgc	aaa	gag	ttt	gtg	aga	aaa	tcg	gct	gcg	caa	tta	atg	720
Ser	Pro	Glu	Arg	Lys	Glu	Phe	Val	Arg	Lys	Ser	Ala	Ala	Gln	Leu	Met	
225					230					235					240	
gaa	acg	att	cgc	aaa	gat	atc	aaa	ccg	cgt	gat	att	gtt	aca	gta	aaa	768
Glu	Thr	Ile	Arg	Lys	Asp	Ile	Lys	Pro	Arg	Asp	Ile	Val	Thr	Val	Lys	
			245						250					255		
gcg	att	gat	aac	gcg	ttt	gca	ctc	gat	atg	gcg	ctc	gga	ggt	tct	aca	816
Ala	Ile	Asp	Asn	Ala	Phe	Ala	Leu	Asp	Met	Ala	Leu	Gly	Gly	Ser	Thr	
			260					265					270			
aat	acc	gtt	ctt	cat	acc	ctt	gcc	ctt	gca	aac	gaa	gcc	ggc	gtt	gaa	864
Asn	Thr	Val	Leu	His	Thr	Leu	Ala	Leu	Ala	Asn	Glu	Ala	Gly	Val	Glu	
		275					280					285				
tac	tct	tta	gaa	cgc	att	aac	gaa	gtc	gct	gag	cgc	gtg	ccg	cac	ttg	912
Tyr	Ser	Leu	Glu	Arg	Ile	Asn	Glu	Val	Ala	Glu	Arg	Val	Pro	His	Leu	
	290					295					300					
gct	aag	ctg	gcg	cct	gca	tcg	gat	gtg	ttt	att	gaa	gat	ctt	cac	gaa	960
Ala	Lys	Leu	Ala	Pro	Ala	Ser	Asp	Val	Phe	Ile	Glu	Asp	Leu	His	Glu	
305					310					315					320	
gcg	ggc	ggc	gtt	tca	gcg	gct	ctg	aat	gag	ctt	tcg	aag	aaa	gaa	gga	1008
Ala	Gly	Gly	Val	Ser	Ala	Ala	Leu	Asn	Glu	Leu	Ser	Lys	Lys	Glu	Gly	
			325					330					335			
gcg	ctt	cat	tta	gat	gcg	ctg	act	gtt	aca	gga	aaa	act	ctt	gga	gaa	1056
Ala	Leu	His	Leu	Asp	Ala	Leu	Thr	Val	Thr	Gly	Lys	Thr	Leu	Gly	Glu	
			340				345						350			
acc	att	gcc	gga	cat	gaa	gta	aag	gat	tat	gac	gtc	att	cac	ccg	ctg	1104
Thr	Ile	Ala	Gly	His	Glu	Val	Lys	Asp	Tyr	Asp	Val	Ile	His	Pro	Leu	
		355					360					365				
gat	caa	cca	ttc	act	gaa	aag	gga	ggc	ctt	gct	gtt	tta	ttc	ggt	aat	1152
Asp	Gln	Pro	Phe	Thr	Glu	Lys	Gly	Gly	Leu	Ala	Val	Leu	Phe	Gly	Asn	
	370					375					380					
cta	gct	ccg	gac	ggc	gct	atc	att	aaa	aca	ggc	ggc	gta	cag	aat	ggg	1200
Leu	Ala	Pro	Asp	Gly	Ala	Ile	Ile	Lys	Thr	Gly	Gly	Val	Gln	Asn	Gly	
385					390					395					400	
att	aca	aga	cac	gaa	ggg	ccg	gct	gtc	gta	ttc	gat	tct	cag	gac	gag	1248
Ile	Thr	Arg	His	Glu	Gly	Pro	Ala	Val	Val	Phe	Asp	Ser	Gln	Asp	Glu	
			405					410					415			

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gcg ctt gac ggc att atc aac cga aaa gta aaa gaa ggc gac gtt gtc	1296
Ala Leu Asp Gly Ile Ile Asn Arg Lys Val Lys Glu Gly Asp Val Val	
420 425 430	
atc atc aga tac gaa ggg cca aaa ggc gga cct ggc atg ccg gaa atg	1344
Ile Ile Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met	
435 440 445	
ctg gcg cca aca tcc caa atc gtt gga atg gga ctc ggg cca aaa gtg	1392
Leu Ala Pro Thr Ser Gln Ile Val Gly Met Gly Leu Gly Pro Lys Val	
450 455 460	
gca ttg att acg gac gga cgt ttt tcc gga gcc tcc cgt ggc ctc tca	1440
Ala Leu Ile Thr Asp Gly Arg Phe Ser Gly Ala Ser Arg Gly Leu Ser	
465 470 475 480	
atc ggc cac gta tca cct gag gcc gct gag ggc ggg ccg ctt gcc ttt	1488
Ile Gly His Val Ser Pro Glu Ala Ala Glu Gly Gly Pro Leu Ala Phe	
485 490 495	
gtt gaa aac gga gac cat att atc gtt gat att gaa aaa cgc atc ttg	1536
Val Glu Asn Gly Asp His Ile Ile Val Asp Ile Glu Lys Arg Ile Leu	
500 505 510	
gat gta caa gtg cca gaa gaa gag tgg gaa aaa cga aaa gcg aac tgg	1584
Asp Val Gln Val Pro Glu Glu Glu Trp Glu Lys Arg Lys Ala Asn Trp	
515 520 525	
aaa ggt ttt gaa ccg aaa gtg aaa acc ggc tac ctg gca cgt tat tct	1632
Lys Gly Phe Glu Pro Lys Val Lys Thr Gly Tyr Leu Ala Arg Tyr Ser	
530 535 540	
aaa ctt gtg aca agt gcc aac acc ggc ggt att atg aaa atc	1674
Lys Leu Val Thr Ser Ala Asn Thr Gly Gly Ile Met Lys Ile	
545 550 555	

<210> 38

<211> 558

<212> PRT

<213> Bacillus subtilis

<400> 38

Met	Ala	Glu	Leu	Arg	Ser	Asn	Met	Ile	Thr	Gln	Gly	Ile	Asp	Arg	Ala
1				5					10					15	

Pro	His	Arg	Ser	Leu	Leu	Arg	Ala	Ala	Gly	Val	Lys	Glu	Glu	Asp	Phe
			20				25						30		

Gly	Lys	Pro	Phe	Ile	Ala	Val	Cys	Asn	Ser	Tyr	Ile	Asp	Ile	Val	Pro
		35					40					45			

Gly	His	Val	His	Leu	Gln	Glu	Phe	Gly	Lys	Ile	Val	Lys	Glu	Ala	Ile
	50					55					60				

Arg	Glu	Ala	Gly	Gly	Val	Pro	Phe	Glu	Phe	Asn	Thr	Ile	Gly	Val	Asp
65					70					75					80

Asp	Gly	Ile	Ala	Met	Gly	His	Ile	Gly	Met	Arg	Tyr	Ser	Leu	Pro	Ser	
				85					90					95		
Arg	Glu	Ile	Ile	Ala	Asp	Ser	Val	Glu	Thr	Val	Val	Ser	Ala	His	Trp	
			100					105					110			
Phe	Asp	Gly	Met	Val	Cys	Ile	Pro	Asn	Cys	Asp	Lys	Ile	Thr	Pro	Gly	
		115					120					125				
Met	Leu	Met	Ala	Ala	Met	Arg	Ile	Asn	Ile	Pro	Thr	Ile	Phe	Val	Ser	
	130					135					140					
Gly	Gly	Pro	Met	Ala	Ala	Gly	Arg	Thr	Ser	Tyr	Gly	Arg	Lys	Ile	Ser	
145					150					155					160	
Leu	Ser	Ser	Val	Phe	Glu	Gly	Val	Gly	Ala	Tyr	Gln	Ala	Gly	Lys	Ile	
				165					170					175		
Asn	Glu	Asn	Glu	Leu	Gln	Glu	Leu	Glu	Gln	Phe	Gly	Cys	Pro	Thr	Cys	
			180					185					190			
Gly	Ser	Cys	Ser	Gly	Met	Phe	Thr	Ala	Asn	Ser	Met	Asn	Cys	Leu	Ser	
		195					200					205				
Glu	Ala	Leu	Gly	Leu	Ala	Leu	Pro	Gly	Asn	Gly	Thr	Ile	Leu	Ala	Thr	
	210					215					220					
Ser	Pro	Glu	Arg	Lys	Glu	Phe	Val	Arg	Lys	Ser	Ala	Ala	Gln	Leu	Met	
225					230					235					240	
Glu	Thr	Ile	Arg	Lys	Asp	Ile	Lys	Pro	Arg	Asp	Ile	Val	Thr	Val	Lys	
				245					250					255		
Ala	Ile	Asp	Asn	Ala	Phe	Ala	Leu	Asp	Met	Ala	Leu	Gly	Gly	Ser	Thr	
			260					265					270			
Asn	Thr	Val	Leu	His	Thr	Leu	Ala	Leu	Ala	Asn	Glu	Ala	Gly	Val	Glu	
		275					280					285				
Tyr	Ser	Leu	Glu	Arg	Ile	Asn	Glu	Val	Ala	Glu	Arg	Val	Pro	His	Leu	
	290					295					300					
Ala	Lys	Leu	Ala	Pro	Ala	Ser	Asp	Val	Phe	Ile	Glu	Asp	Leu	His	Glu	
305					310					315					320	
Ala	Gly	Gly	Val	Ser	Ala	Ala	Leu	Asn	Glu	Leu	Ser	Lys	Lys	Glu	Gly	
				325					330					335		
Ala	Leu	His	Leu	Asp	Ala	Leu	Thr	Val	Thr	Gly	Lys	Thr	Leu	Gly	Glu	
			340					345					350			
Thr	Ile	Ala	Gly	His	Glu	Val	Lys	Asp	Tyr	Asp	Val	Ile	His	Pro	Leu	
		355					360					365				
Asp	Gln	Pro	Phe	Thr	Glu	Lys	Gly	Gly	Leu	Ala	Val	Leu	Phe	Gly	Asn	
	370					375					380					

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Leu Ala Pro Asp Gly Ala Ile Ile Lys Thr Gly Gly Val Gln Asn Gly
 385 390 395 400
 Ile Thr Arg His Glu Gly Pro Ala Val Val Phe Asp Ser Gln Asp Glu
 405 410 415
 Ala Leu Asp Gly Ile Ile Asn Arg Lys Val Lys Glu Gly Asp Val Val
 420 425 430
 Ile Ile Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met
 435 440 445
 Leu Ala Pro Thr Ser Gln Ile Val Gly Met Gly Leu Gly Pro Lys Val
 450 455 460
 Ala Leu Ile Thr Asp Gly Arg Phe Ser Gly Ala Ser Arg Gly Leu Ser
 465 470 475 480
 Ile Gly His Val Ser Pro Glu Ala Ala Glu Gly Gly Pro Leu Ala Phe
 485 490 495
 Val Glu Asn Gly Asp His Ile Ile Val Asp Ile Glu Lys Arg Ile Leu
 500 505 510
 Asp Val Gln Val Pro Glu Glu Glu Trp Glu Lys Arg Lys Ala Asn Trp
 515 520 525
 Lys Gly Phe Glu Pro Lys Val Lys Thr Gly Tyr Leu Ala Arg Tyr Ser
 530 535 540
 Lys Leu Val Thr Ser Ala Asn Thr Gly Gly Ile Met Lys Ile
 545 550 555

<210> 39

<211> 194

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:promoter
sequence

<220>

<221> -35_signal

<222> (136)..(141)

<220>

<221> -10_signal

<222> (159)..(164)

<400> 39

gctattgacg acagctatgg ttcaactgtcc accaaccaaa actgtgctca gtaccgccaa 60

tattttctccc ttgaggggta caaagaggtg tccctagaag agatccacgc tgtgtataaaa 120

ttttacaaaa aggtattgac tttccctaca ggggtgtgtaa taatttaatt acaggcgggg 180

gcaaccccg c t g t

194

<210> 40

<211> 163

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: promoter
sequence

<220>

<221> -35_signal

<222> (113)..(118)

<220>

<221> -10_signal

<222> (136)..(141)

<400> 40

gcctacctag cttccaagaa agatattccta acagcacaag agcggaaaga tgttttgttc 60

tacatccaga acaacctctg ctaaaattcc tgaaaaattt tgcaaaaagt tgttgacttt 120

atctacaagg tgtggtataa taatcttaac aacagcagga cgc

163

<210> 41

<211> 127

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: promoter
sequence

<220>

<221> -35_signal

<222> (34)..(39)

<220>

<221> -10_signal

<222> (58)..(63)

<220>

<221> -35_signal

<222> (75)..(80)

<220>

<221> -10_signal

<222> (98)..(103)

<400> 41

gaggaatcat agaattttgt caaaataatt ttattgacaa cgtcttatta acgttgatat 60

aatttaaatt ttatttgaca aaaatgggct cgtgttgtag aataaatgta gtgaggtgga 120

tgcaatg

127

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 42

taaacaatgag gaggagaaaa catg

24

<210> 43

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 43

attcgagaaa tggagagaat ataatatg

28

<210> 44

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 44

agaaaggagg tga

13

<210> 45

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 45

ttaagaaagg aggtgannnn atg

23

<210> 46

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome

- 51 -

binding site

<400> 46
ttagaaagga ggtgannnnn atg 23

<210> 47
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 47
agaaaggagg tgannnnnnn atg 23

<210> 48
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 48
agaaaggagg tgannnnnna tg 22

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 49
ccctctagaa ggaggagaaa acatg 25

<210> 50
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 50
ccctctagag gaggagaaaa catg 24

<210> 51
<211> 23
<212> DNA

- 52 -

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 51

ttagaaagga ggattttaa atg

23

<210> 52

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 52

ttagaaagga ggtttaatta atg

23

<210> 53

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 53

ttagaaagga ggtgatttaa atg

23

<210> 54

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 54

ttagaaagga ggtgtttaaa atg

23

<210> 55

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 55

attcgagaaa ggaggtgaat ataatatg

28

<210> 56

- 53 -

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 56

attcgagaaa ggaggtgaat aataatg

27

<210> 57

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 57

attcgtagaa aggaggtgaa ttaatatg

28

<210> 58

<211> 3291

<212> DNA

<213> Bacillus subtilis

<400> 58

atgggggacta atgtacaggt ggattcagca tctgccgaat gtacacagac gatgagcgga 60
gcattaatgc tgattgaatc attaaaaaaa gagaaagtag aaatgatctt cggttatccg 120
ggcgggggctg tgcttccgat ttacgataag ctatacaatt cagggttggg acatatacctt 180
ccccgtcacg aacaaggagc aattcatgca gcggagggat acgcaagggt ctccggaaaa 240
ccgggtgtcg tcattgccac gtcaggggccg ggagcgacaa accttggttac aggccttgct 300
gatgccatga ttgattcatt gccgttagtc gtctttacag ggcaggtagc aacctctgta 360
atcgggagcg atgcatttca ggaagcagac attttaggga ttacgatgcc agtaacaaaa 420
cacagctacc aggttcgcca gccggaagat ctgccgcgca tcattaaaga agcgttccat 480
attgcaacaa ctggaagacc cggacctgta ttgattgata ttccgaaga tgtagcaaca 540
attgaaggag aattcagcta cgatcatgag atgaatctcc cgggatacca gccgacaaca 600
gagccgaatt atttgcagat ccgcaagctt gtggaagccg tgagcagtgc gaaaaaaccg 660
gtgatcctgg cgggtgcggg cgtactgcac ggaaaagcgt cagaagaatt aaaaaattat 720
gctgaacagc agcaaataccc tgtggcacac acccttttgg ggctcggagg cttcccggct 780
gaccatccgc ttttcctagg gatggcggga atgcacggta cttatacagc caatatggcc 840

cttcatgaat gtgatctatt aatcagtatc ggcgcccggt ttgatgaccg tgtcacagga 900
aacctgaaac actttgccag aaacgcaaag atagcccaca tcgatattga tccagctgaa 960
atcggaaaaa tcatgaaaac acagattcct gtagtcggag acagcaaaat tgtcctgcag 1020
gagctgatca aacaagacgg caaacaagc gattcaagcg aatggaaaaa acagctcgca 1080
gaatggaaag aagagtatcc gctctgggtat gtagataatg aagaagaagg ttttaaacct 1140
cagaaattga ttgaatatat tcatcaattt acaaaaggag aggccattgt cgcaacggat 1200
gtaggccagc atcaaattgt gtcagcgcaa ttttatccgt tccaaaaagc agataaatgg 1260
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gaatctaaat tcgcttctca gcctgacttc gtcaaattgt ccgaagcata cggcattaaa 1560
ggcatcagaa tttcatcaga agcgggaagc aaggaaaagc tggaagaggc attaacatca 1620
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tgactgtggt gaaccgctcc ggggtgttaa accggatcac cggctctattc aaaaaaggc 1800
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ccttcgtcgt tcatgttgaa ggtgaaaatg atgttgaaca gttaacgaaa cagctcaaca 1920
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tggccttaat caaggttgtc tccgcacctt caacaagaac agagattaat ggaatcatag 2040
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aacaatatct attgtataaa acataacaag ggagagattg aaatggtaaa agtatattat 2280
aacggtgata tcaaagagaa cgtattggct ggaaaaacag tagcggttat cgggtacggt 2340
tcgcaaggcc acgcacatgc cctgaacctt aaagaaagcg gagtagacgt gatcgctcgt 2400
gttagacaag gaaaatcttt cactcaagcc caagaagacg gacataaagt attttcagta 2460
aaagaagcgg cagccaagc cgaaatcatc atggttctgc ttccggatga gcagcagcaa 2520
aaagtatacg aagctgaaat caaagatgaa ttgacagcag gaaaatcatt agtattcgct 2580

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catggattta acgtgcattt ccatacaatt gttcctccgg cggatgtaga tgtattctta 2640
 gtggccccta aaggcccggg acacttggta agaagaacat atgagcaagg agctggcgta 2700
 cctgcattgt tcgcaatcta tcaagatgtg actggagaag caagagacaa agccctcgct 2760
 tatgctaaag gaatcggcgg cgcaagagcg ggcgtattag aaacgacatt taaagaagaa 2820
 acagaaacag atttgttcgg tgagcaagca gttctttgcg gcggattaag cgcgcttgct 2880
 aaagccggat ttgaaacctt aactgaagca ggttatcagc ctgaacttgc atacttcgag 2940
 tgtcttcattg agctgaaatt aatcgtagac cttatgtacg aagaaggact tgcaggaatg 3000
 agatattcaa tctctgacac agcacagtgg ggagatttcg tatcaggccc tcgcgttggtg 3060
 gacgccaaag taaaagaatc tatgaaagaa gtattaaaag atatccaaaa cggtaacattc 3120
 gcaaaagagt ggatcgtcga aaaccaagta aaccgtcctc gtttcaacgc tatcaatgca 3180
 agcgagaacg aacatcaaatt cgaagtagtg ggaagaaagc ttcgtgaaat gatgccgttt 3240
 gtgaaacaag gcaagaagaa ggaagcgggtg gtctccgttg cgcaaaatta a 3291

<210> 59

<211> 2363

<212> DNA

<213> *Bacillus subtilis*

<220>

<221> CDS

<222> (242)..(1072)

<220>

<221> CDS

<222> (1077)..(1934)

<220>

<221> CDS

<222> (1939)..(2319)

<400> 59

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 cctattatta aaatagatag acattgcagc agtctgcctt gatccaaaaa aggactggga 120
 cagagggatg aaactcgccg aacttttagaa agtgaagaat ccttctcggt gtaacggaag 180
 gttttttggc ttgcagaaga aaacggcaga tcatctcctc taaacatgag gaggagaaaa 240
 c atg aaa aca aaa ctg gat ttt cta aaa atg aag gag tct gaa gaa ccg 289
 Met Lys Thr Lys Leu Asp Phe Leu Lys Met Lys Glu Ser Glu Glu Pro
 1 5 10 15

att gtc atg ctg acc gct tat gat tat ccg gca gct aaa ctt gct gaa 337
 Ile Val Met Leu Thr Ala Tyr Asp Tyr Pro Ala Ala Lys Leu Ala Glu

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20							25					30					
caa	gcg	gga	gtt	gac	atg	att	tta	gtc	ggt	gat	tca	ctt	gga	atg	gtc	385	
Gln	Ala	Gly	Val	Asp	Met	Ile	Leu	Val	Gly	Asp	Ser	Leu	Gly	Met	Val		
		35					40					45					
gtc	ctc	ggc	ctt	gat	tca	act	gtc	ggt	gtg	aca	gtt	gcg	gac	atg	atc	433	
Val	Leu	Gly	Leu	Asp	Ser	Thr	Val	Gly	Val	Thr	Val	Ala	Asp	Met	Ile		
	50					55					60						
cat	cat	aca	aaa	gcc	gtt	aaa	agg	ggt	gcg	ccg	aat	acc	ttt	att	gtg	481	
His	His	Thr	Lys	Ala	Val	Lys	Arg	Gly	Ala	Pro	Asn	Thr	Phe	Ile	Val		
65					70					75					80		
aca	gat	atg	ccg	ttt	atg	tct	tat	cac	ctg	tct	aag	gaa	gat	acg	ctg	529	
Thr	Asp	Met	Pro	Phe	Met	Ser	Tyr	His	Leu	Ser	Lys	Glu	Asp	Thr	Leu		
				85					90					95			
aaa	aat	gca	gcg	gct	atc	gtt	cag	gaa	agc	gga	gct	gac	gca	ctg	aag	577	
Lys	Asn	Ala	Ala	Ala	Ile	Val	Gln	Glu	Ser	Gly	Ala	Asp	Ala	Leu	Lys		
			100					105					110				
ctt	gag	ggc	gga	gaa	ggc	gtg	ttt	gaa	tcc	att	cgc	gca	ttg	acg	ctt	625	
Leu	Glu	Gly	Gly	Glu	Gly	Val	Phe	Glu	Ser	Ile	Arg	Ala	Leu	Thr	Leu		
		115					120					125					
gga	ggc	att	cca	gta	gtc	agt	cac	tta	ggt	ttg	aca	ccg	cag	tca	gtc	673	
Gly	Gly	Ile	Pro	Val	Val	Ser	His	Leu	Gly	Leu	Thr	Pro	Gln	Ser	Val		
		130				135					140						
ggc	gta	ctg	ggc	ggc	tat	aaa	gta	cag	ggc	aaa	gac	gaa	caa	agc	gcc	721	
Gly	Val	Leu	Gly	Gly	Tyr	Lys	Val	Gln	Gly	Lys	Asp	Glu	Gln	Ser	Ala		
145					150					155					160		
aaa	aaa	tta	ata	gaa	gac	agt	ata	aaa	tgc	gaa	gaa	gca	gga	gct	atg	769	
Lys	Lys	Leu	Ile	Glu	Asp	Ser	Ile	Lys	Cys	Glu	Glu	Ala	Gly	Ala	Met		
				165					170					175			
atg	ctt	gtg	ctg	gaa	tgt	gtg	ccg	gca	gaa	ctc	aca	gcc	aaa	att	gcc	817	
Met	Leu	Val	Leu	Glu	Cys	Val	Pro	Ala	Glu	Leu	Thr	Ala	Lys	Ile	Ala		
			180					185					190				
gag	acg	cta	agc	ata	ccg	gtc	att	gga	atc	ggg	gct	ggt	gtg	aaa	gcg	865	
Glu	Thr	Leu	Ser	Ile	Pro	Val	Ile	Gly	Ile	Gly	Ala	Gly	Val	Lys	Ala		
		195					200					205					
gac	gga	caa	gtt	ctc	gtt	tat	cat	gat	att	atc	ggc	cac	ggt	gtt	gag	913	
Asp	Gly	Gln	Val	Leu	Val	Tyr	His	Asp	Ile	Ile	Gly	His	Gly	Val	Glu		
	210					215					220						
aga	aca	cct	aaa	ttt	gta	aag	caa	tat	acg	cgc	att	gat	gaa	acc	atc	961	
Arg	Thr	Pro	Lys	Phe	Val	Lys	Gln	Tyr	Thr	Arg	Ile	Asp	Glu	Thr	Ile		
225					230					235					240		
gaa	aca	gca	atc	agc	gga	tat	gtt	cag	gat	gta	aga	cat	cgt	gct	ttc	1009	
Glu	Thr	Ala	Ile	Ser	Gly	Tyr	Val	Gln	Asp	Val	Arg	His	Arg	Ala	Phe		
				245					250					255			

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cct gaa caa aag cat tcc ttt caa atg aac cag aca gtg ctt gac ggc	1057
Pro Glu Gln Lys His Ser Phe Gln Met Asn Gln Thr Val Leu Asp Gly	
260 265 270	
ttg tac ggg gga aaa taag atg aga cag att act gat att tca cag ctg	1106
Leu Tyr Gly Gly Lys Met Arg Gln Ile Thr Asp Ile Ser Gln Leu	
275 280 285	
aaa gaa gcc ata aaa caa tac cat tca gag ggc aag tca atc gga ttt	1154
Lys Glu Ala Ile Lys Gln Tyr His Ser Glu Gly Lys Ser Ile Gly Phe	
290 295 300	
gtt ccg acg atg ggg ttt ctg cat gag ggg cat tta acc tta gca gac	1202
Val Pro Thr Met Gly Phe Leu His Glu Gly His Leu Thr Leu Ala Asp	
305 310 315	
aaa gca aga caa gaa aac gac gcc gtt att atg agt att ttt gtg aat	1250
Lys Ala Arg Gln Glu Asn Asp Ala Val Ile Met Ser Ile Phe Val Asn	
320 325 330 335	
cct gca caa ttc ggc cct aat gaa gat ttt gaa gca tat ccg cgc gat	1298
Pro Ala Gln Phe Gly Pro Asn Glu Asp Phe Glu Ala Tyr Pro Arg Asp	
340 345 350	
att gag cgg gat gca gct ctt gca gaa aac gcc gga gtc gat att ctt	1346
Ile Glu Arg Asp Ala Ala Leu Ala Glu Asn Ala Gly Val Asp Ile Leu	
355 360 365	
ttt acg cca gat gct cat gat atg tat ccc ggt gaa aag aat gtc acg	1394
Phe Thr Pro Asp Ala His Asp Met Tyr Pro Gly Glu Lys Asn Val Thr	
370 375 380	
att cat gta gaa aga cgc aca gac gtg tta tgc ggg cgc tca aga gaa	1442
Ile His Val Glu Arg Arg Thr Asp Val Leu Cys Gly Arg Ser Arg Glu	
385 390 395	
gga cat ttt gac ggg gtc gcg atc gta ctg acg aag ctt ttc aat cta	1490
Gly His Phe Asp Gly Val Ala Ile Val Leu Thr Lys Leu Phe Asn Leu	
400 405 410 415	
gtc aag ccg act cgt gcc tat ttc ggt tta aaa gat gcg cag cag gta	1538
Val Lys Pro Thr Arg Ala Tyr Phe Gly Leu Lys Asp Ala Gln Gln Val	
420 425 430	
gct gtt gtt gat ggg tta atc agc gac ttc ttc atg gat att gaa ttg	1586
Ala Val Val Asp Gly Leu Ile Ser Asp Phe Phe Met Asp Ile Glu Leu	
435 440 445	
gtt cct gtc gat acg gtc aga gag gaa gac ggc tta gcc aaa agc tct	1634
Val Pro Val Asp Thr Val Arg Glu Glu Asp Gly Leu Ala Lys Ser Ser	
450 455 460	
cgc aat gta tac tta aca gct gag gaa aga aaa gaa gcg cct aag ctg	1682
Arg Asn Val Tyr Leu Thr Ala Glu Glu Arg Lys Glu Ala Pro Lys Leu	
465 470 475	
tat cgg gcc ctt caa aca agt gcg gaa ctt gtc caa gcc ggt gaa aga	1730
Tyr Arg Ala Leu Gln Thr Ser Ala Glu Leu Val Gln Ala Gly Glu Arg	

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480		485		490		495	
gat cct gaa gcg gtg	ata aaa gct gca aaa gat atc att gaa acg act	1778					
Asp Pro Glu Ala Val	Ile Lys Ala Ala Lys Asp Ile Ile Glu Thr Thr						
	500 505 510						
agc gga acc ata gac tat gta gag ctt tat tcc tat ccg gaa ctc gag	1826						
Ser Gly Thr Ile Asp Tyr Val Glu Leu Tyr Ser Tyr Pro Glu Leu Glu							
	515 520 525						
cct gtg aat gaa att gct gga aag atg att ctc gct gtt gca gtt gct	1874						
Pro Val Asn Glu Ile Ala Gly Lys Met Ile Leu Ala Val Ala Val Ala							
	530 535 540						
ttt tca aaa gcg cgt tta ata gat aat atc att att gat att cga gaa	1922						
Phe Ser Lys Ala Arg Leu Ile Asp Asn Ile Ile Ile Asp Ile Arg Glu							
	545 550 555						
atg gag aga ata taat atg tat cga aca atg atg agc ggc aaa ctt cac	1971						
Met Glu Arg Ile Met Tyr Arg Thr Met Met Ser Gly Lys Leu His							
	560 565 570						
agg gca act gtt acg gaa gca aac ctg aac tat gtg gga agc att aca	2019						
Arg Ala Thr Val Thr Glu Ala Asn Leu Asn Tyr Val Gly Ser Ile Thr							
	575 580 585 590						
att gat gaa gat ctc att gat gct gtg gga atg ctt cct aat gaa aaa	2067						
Ile Asp Glu Asp Leu Ile Asp Ala Val Gly Met Leu Pro Asn Glu Lys							
	595 600 605						
gta caa att gtg aat aat aat aat gga gca cgt ctt gaa acg tat att	2115						
Val Gln Ile Val Asn Asn Asn Asn Gly Ala Arg Leu Glu Thr Tyr Ile							
	610 615 620						
att cct ggt aaa cgg gga agc ggc gtc ata tgc tta aac ggt gca gcc	2163						
Ile Pro Gly Lys Arg Gly Ser Gly Val Ile Cys Leu Asn Gly Ala Ala							
	625 630 635						
gca cgc ctt gtg cag gaa gga gat aag gtc att att att tcc tac aaa	2211						
Ala Arg Leu Val Gln Glu Gly Asp Lys Val Ile Ile Ile Ser Tyr Lys							
	640 645 650						
atg atg tct gat caa gaa gcg gca agc cat gag ccg aaa gtg gct gtt	2259						
Met Met Ser Asp Gln Glu Ala Ala Ser His Glu Pro Lys Val Ala Val							
	655 660 665 670						
ctg aat gat caa aac aaa att gaa caa atg ctg ggg aac gaa cca gcc	2307						
Leu Asn Asp Gln Asn Lys Ile Glu Gln Met Leu Gly Asn Glu Pro Ala							
	675 680 685						
cgt aca att ttg tagaagaaaa gcccccttta tcgggggttt tcttttaaga tttt	2363						
Arg Thr Ile Leu							
	690						

<210> 60
 <211> 293
 <212> PRT

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<213> Bacillus subtilis

<400> 60

Met	Ser	Ile	Ala	Val	Ser	Glu	Glu	Glu	Ala	Lys	Ala	Val	Glu	Gly	Leu	1	5	10	15
Asn	Asp	Tyr	Leu	Ser	Val	Glu	Glu	Val	Glu	Thr	Ile	Tyr	Ile	Pro	Leu	20	25	30	
Val	Arg	Leu	Leu	His	Leu	His	Val	Lys	Ser	Ala	Ala	Glu	Arg	Asn	Lys	35	40	45	
His	Val	Asn	Val	Phe	Leu	Lys	His	Pro	His	Ser	Ala	Lys	Ile	Pro	Phe	50	55	60	
Ile	Ile	Gly	Ile	Ala	Gly	Ser	Val	Ala	Val	Gly	Lys	Ser	Thr	Thr	Ala	65	70	75	80
Arg	Ile	Leu	Gln	Lys	Leu	Leu	Ser	Arg	Leu	Pro	Asp	Arg	Pro	Lys	Val	85	90	95	
Ser	Leu	Ile	Thr	Thr	Asp	Gly	Phe	Leu	Phe	Pro	Thr	Ala	Glu	Leu	Lys	100	105	110	
Lys	Lys	Asn	Met	Met	Ser	Arg	Lys	Gly	Phe	Pro	Glu	Ser	Tyr	Asp	Val	115	120	125	
Lys	Ala	Leu	Leu	Glu	Phe	Leu	Asn	Asp	Leu	Lys	Ser	Gly	Lys	Asp	Ser	130	135	140	
Val	Lys	Ala	Pro	Val	Tyr	Ser	His	Leu	Thr	Tyr	Asp	Arg	Glu	Glu	Gly	145	150	155	160
Val	Phe	Glu	Val	Val	Glu	Gln	Ala	Asp	Ile	Val	Ile	Ile	Glu	Gly	Ile	165	170	175	
Asn	Val	Leu	Gln	Ser	Pro	Thr	Leu	Glu	Asp	Asp	Arg	Glu	Asn	Pro	Arg	180	185	190	
Ile	Phe	Val	Ser	Asp	Phe	Phe	Asp	Phe	Ser	Ile	Tyr	Val	Asp	Ala	Glu	195	200	205	
Glu	Ser	Arg	Ile	Phe	Thr	Trp	Tyr	Leu	Glu	Arg	Phe	Arg	Leu	Leu	Arg	210	215	220	
Glu	Thr	Ala	Phe	Gln	Asn	Pro	Asp	Ser	Tyr	Phe	His	Lys	Phe	Lys	Asp	225	230	235	240
Leu	Ser	Asp	Gln	Glu	Ala	Asp	Glu	Met	Ala	Ala	Ser	Ile	Trp	Glu	Ser	245	250	255	
Val	Asn	Arg	Pro	Asn	Leu	Tyr	Glu	Asn	Ile	Leu	Pro	Thr	Lys	Phe	Arg	260	265	270	
Ser	Asp	Leu	Ile	Leu	Arg	Lys	Gly	Asp	Gly	His	Lys	Val	Glu	Glu	Val	275	280	285	
Leu	Val	Arg	Arg	Val															

- 60 -

290

<210> 61

<211> 281

<212> PRT

<213> Bacillus subtilis

<400> 61

Met	Glu	Gly	Leu	Asn	Asp	Tyr	Leu	Ser	Val	Glu	Glu	Val	Glu	Thr	Ile	1	5	10	15
Tyr	Ile	Pro	Leu	Val	Arg	Leu	Leu	His	Leu	His	Val	Lys	Ser	Ala	Ala	20	25	30	
Glu	Arg	Asn	Lys	His	Val	Asn	Val	Phe	Leu	Lys	His	Pro	His	Ser	Ala	35	40	45	
Lys	Ile	Pro	Phe	Ile	Ile	Gly	Ile	Ala	Gly	Ser	Val	Ala	Val	Gly	Lys	50	55	60	
Ser	Thr	Thr	Ala	Arg	Ile	Leu	Gln	Lys	Leu	Leu	Ser	Arg	Leu	Pro	Asp	65	70	75	80
Arg	Pro	Lys	Val	Ser	Leu	Ile	Thr	Thr	Asp	Gly	Phe	Leu	Phe	Pro	Thr	85	90	95	
Ala	Glu	Leu	Lys	Lys	Lys	Asn	Met	Met	Ser	Arg	Lys	Gly	Phe	Pro	Glu	100	105	110	
Ser	Tyr	Asp	Val	Lys	Ala	Leu	Leu	Glu	Phe	Leu	Asn	Asp	Leu	Lys	Ser	115	120	125	
Gly	Lys	Asp	Ser	Val	Lys	Ala	Pro	Val	Tyr	Ser	His	Leu	Thr	Tyr	Asp	130	135	140	
Arg	Glu	Glu	Gly	Val	Phe	Glu	Val	Val	Glu	Gln	Ala	Asp	Ile	Val	Ile	145	150	155	160
Ile	Glu	Gly	Ile	Asn	Val	Leu	Gln	Ser	Pro	Thr	Leu	Glu	Asp	Asp	Arg	165	170	175	
Glu	Asn	Pro	Arg	Ile	Phe	Val	Ser	Asp	Phe	Phe	Asp	Phe	Ser	Ile	Tyr	180	185	190	
Val	Asp	Ala	Glu	Glu	Ser	Arg	Ile	Phe	Thr	Trp	Tyr	Leu	Glu	Arg	Phe	195	200	205	
Arg	Leu	Leu	Arg	Glu	Thr	Ala	Phe	Gln	Asn	Pro	Asp	Ser	Tyr	Phe	His	210	215	220	
Lys	Phe	Lys	Asp	Leu	Ser	Asp	Gln	Glu	Ala	Asp	Glu	Met	Ala	Ala	Ser	225	230	235	240
Ile	Trp	Glu	Ser	Val	Asn	Arg	Pro	Asn	Leu	Tyr	Glu	Asn	Ile	Leu	Pro	245	250	255	
Thr	Lys	Phe	Arg	Ser	Asp	Leu	Ile	Leu	Arg	Lys	Gly	Asp	Gly	His	Lys				

- 61 -

260 265 270
 Val Glu Glu Val Leu Val Arg Arg Val
 275 280

<210> 62
 <211> 1092
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(1089)

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 Met Thr Lys Gln Thr Ile Arg Val Glu Leu Thr Ser Thr Lys Lys Pro
 1 5 10 15
 aaa cca gac cca aat cag ctt tcg ttc gga aga gtg ttt aca gac cac 96
 Lys Pro Asp Pro Asn Gln Leu Ser Phe Gly Arg Val Phe Thr Asp His
 20 25 30
 atg ttt gta atg gac tat gcc gca gat aaa ggt tgg tac gat cca aga 144
 Met Phe Val Met Asp Tyr Ala Ala Asp Lys Gly Trp Tyr Asp Pro Arg
 35 40 45
 atc att cct tat caa ccc tta tca atg gat cca act gca atg gtc tat 192
 Ile Ile Pro Tyr Gln Pro Leu Ser Met Asp Pro Thr Ala Met Val Tyr
 50 55 60
 cac tac ggc caa acc gtg ttt gaa ggg tta aag gct tac gtg tca gag 240
 His Tyr Gly Gln Thr Val Phe Glu Gly Leu Lys Ala Tyr Val Ser Glu
 65 70 75 80
 gat gac cat gtt ctg ctt ttc aga ccg gaa aaa aat atg gaa cgc ctg 288
 Asp Asp His Val Leu Leu Phe Arg Pro Glu Lys Asn Met Glu Arg Leu
 85 90 95
 aat caa tca aac gac cgc ctc tgc atc ccg caa att gat gaa gaa cag 336
 Asn Gln Ser Asn Asp Arg Leu Cys Ile Pro Gln Ile Asp Glu Glu Gln
 100 105 110
 gtt ctt gaa ggc tta aag cag ctt gtc gca att gat aaa gac tgg att 384
 Val Leu Glu Gly Leu Lys Gln Leu Val Ala Ile Asp Lys Asp Trp Ile
 115 120 125
 cca aat gcg gag ggc acg tcc ctt tac atc cgt ccg ttc atc atc gca 432
 Pro Asn Ala Glu Gly Thr Ser Leu Tyr Ile Arg Pro Phe Ile Ile Ala
 130 135 140
 acc gag cct ttc ctt ggt gtt gcg gca tct cat acg tat aag ctc ttg 480
 Thr Glu Pro Phe Leu Gly Val Ala Ala Ser His Thr Tyr Lys Leu Leu
 145 150 155 160
 atc att ctt tct ccg gtc ggc tct tat tac aaa gaa ggc att aag ccg 528
 Ile Ile Leu Ser Pro Val Gly Ser Tyr Tyr Lys Glu Gly Ile Lys Pro

- 62 -

										165			170			175			
gtc	aaa	atc	gct	ggt	gaa	agt	gaa	ttt	gtc	cgt	gcg	gta	aaa	ggc	gga		576		
Val	Lys	Ile	Ala	Val	Glu	Ser	Glu	Phe	Val	Arg	Ala	Val	Lys	Gly	Gly				
			180				185						190						
aca	gga	aat	gcc	aaa	acc	gca	gga	aac	tat	gct	tca	agc	tta	aaa	gcg		624		
Thr	Gly	Asn	Ala	Lys	Thr	Ala	Gly	Asn	Tyr	Ala	Ser	Ser	Leu	Lys	Ala				
			195				200						205						
cag	cag	gta	gcc	gaa	gag	aaa	gga	ttt	tct	caa	gta	ctc	tgg	ctg	gac		672		
Gln	Gln	Val	Ala	Glu	Glu	Lys	Gly	Phe	Ser	Gln	Val	Leu	Trp	Leu	Asp				
			210				215						220						
ggc	att	gag	aag	aaa	tac	atc	gaa	gaa	gtc	gga	agc	atg	aac	atc	ttc		720		
Gly	Ile	Glu	Lys	Lys	Tyr	Ile	Glu	Glu	Val	Gly	Ser	Met	Asn	Ile	Phe				
			225				230						235			240			
ttc	aaa	atc	aac	ggt	gaa	atc	gta	aca	ccg	atg	ctg	aac	ggg	agc	atc		768		
Phe	Lys	Ile	Asn	Gly	Glu	Ile	Val	Thr	Pro	Met	Leu	Asn	Gly	Ser	Ile				
			245				250						255						
ctg	gaa	ggc	att	acg	cgc	aat	tca	gtc	atc	gcc	ttg	ctt	aag	cat	tgg		816		
Leu	Glu	Gly	Ile	Thr	Arg	Asn	Ser	Val	Ile	Ala	Leu	Leu	Lys	His	Trp				
			260				265						270						
ggc	ctt	caa	ggt	tca	gaa	cga	aaa	att	gcg	atc	gat	gag	gtc	atc	caa		864		
Gly	Leu	Gln	Val	Ser	Glu	Arg	Lys	Ile	Ala	Ile	Asp	Glu	Val	Ile	Gln				
			275				280						285						
gcc	cat	aaa	gac	ggc	atc	ctg	gaa	gaa	gcc	ttc	gga	aca	ggt	aca	gca		912		
Ala	His	Lys	Asp	Gly	Ile	Leu	Glu	Glu	Ala	Phe	Gly	Thr	Gly	Thr	Ala				
			290				295						300						
gct	ggt	att	tcc	cca	gtc	ggc	gag	ctg	atc	tgg	cag	gat	gaa	aca	ctt		960		
Ala	Val	Ile	Ser	Pro	Val	Gly	Glu	Leu	Ile	Trp	Gln	Asp	Glu	Thr	Leu				
			305				310						315			320			
tcg	atc	aac	aac	ggt	gaa	aca	gga	gaa	atc	gca	aaa	aaa	cta	tat	gac		1008		
Ser	Ile	Asn	Asn	Gly	Glu	Thr	Gly	Glu	Ile	Ala	Lys	Lys	Leu	Tyr	Asp				
			325				330						335						
acg	att	aca	ggc	att	caa	aaa	ggc	gct	gtc	gca	gac	gaa	ttc	gga	tgg		1056		
Thr	Ile	Thr	Gly	Ile	Gln	Lys	Gly	Ala	Val	Ala	Asp	Glu	Phe	Gly	Trp				
			340				345						350						
acg	acc	gaa	gtc	gca	gcg	ctg	act	gaa	agc	aag	taa						1092		
Thr	Thr	Glu	Val	Ala	Ala	Leu	Thr	Glu	Ser	Lys									
			355				360												

<210> 63

<211> 363

<212> PRT

<213> Bacillus subtilis

<400> 63

Met Thr Lys Gln Thr Ile Arg Val Glu Leu Thr Ser Thr Lys Lys Pro

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1	5	10	15
Lys Pro Asp Pro Asn Gln Leu Ser Phe Gly Arg Val Phe Thr Asp His	20	25	30
Met Phe Val Met Asp Tyr Ala Ala Asp Lys Gly Trp Tyr Asp Pro Arg	35	40	45
Ile Ile Pro Tyr Gln Pro Leu Ser Met Asp Pro Thr Ala Met Val Tyr	50	55	60
His Tyr Gly Gln Thr Val Phe Glu Gly Leu Lys Ala Tyr Val Ser Glu	65	70	75
Asp Asp His Val Leu Leu Phe Arg Pro Glu Lys Asn Met Glu Arg Leu	85	90	95
Asn Gln Ser Asn Asp Arg Leu Cys Ile Pro Gln Ile Asp Glu Glu Gln	100	105	110
Val Leu Glu Gly Leu Lys Gln Leu Val Ala Ile Asp Lys Asp Trp Ile	115	120	125
Pro Asn Ala Glu Gly Thr Ser Leu Tyr Ile Arg Pro Phe Ile Ile Ala	130	135	140
Thr Glu Pro Phe Leu Gly Val Ala Ala Ser His Thr Tyr Lys Leu Leu	145	150	155
Ile Ile Leu Ser Pro Val Gly Ser Tyr Tyr Lys Glu Gly Ile Lys Pro	165	170	175
Val Lys Ile Ala Val Glu Ser Glu Phe Val Arg Ala Val Lys Gly Gly	180	185	190
Thr Gly Asn Ala Lys Thr Ala Gly Asn Tyr Ala Ser Ser Leu Lys Ala	195	200	205
Gln Gln Val Ala Glu Glu Lys Gly Phe Ser Gln Val Leu Trp Leu Asp	210	215	220
Gly Ile Glu Lys Lys Tyr Ile Glu Glu Val Gly Ser Met Asn Ile Phe	225	230	235
Phe Lys Ile Asn Gly Glu Ile Val Thr Pro Met Leu Asn Gly Ser Ile	245	250	255
Leu Glu Gly Ile Thr Arg Asn Ser Val Ile Ala Leu Leu Lys His Trp	260	265	270
Gly Leu Gln Val Ser Glu Arg Lys Ile Ala Ile Asp Glu Val Ile Gln	275	280	285
Ala His Lys Asp Gly Ile Leu Glu Glu Ala Phe Gly Thr Gly Thr Ala	290	295	300
Ala Val Ile Ser Pro Val Gly Glu Leu Ile Trp Gln Asp Glu Thr Leu	305	310	315
			320

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Ser	Ile	Asn	Asn	Gly	Glu	Thr	Gly	Glu	Ile	Ala	Lys	Lys	Leu	Tyr	Asp
				325					330					335	
Thr	Ile	Thr	Gly	Ile	Gln	Lys	Gly	Ala	Val	Ala	Asp	Glu	Phe	Gly	Trp
			340					345					350		
Thr	Thr	Glu	Val	Ala	Ala	Leu	Thr	Glu	Ser	Lys					
		355					360								

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<211> 1071
<212> DNA
<213> Bacillus subtilis
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<220>
<221> CDS
<222> (1) .. (1068)
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Met	Asn	Lys	Leu	Ile	Glu	Arg	Glu	Lys	Thr	Val	Tyr	Tyr	Lys	Glu	Lys	
1				5					10					15		
ccc	gac	ccg	tct	tcc	ttg	ggg	ttt	gga	caa	tat	ttt	aca	gat	tat	atg	96
Pro	Asp	Pro	Ser	Ser	Leu	Gly	Phe	Gly	Gln	Tyr	Phe	Thr	Asp	Tyr	Met	
			20					25					30			
ttt	gtg	atg	gac	tac	gaa	gag	ggg	att	gga	tgg	cat	cat	ccg	aga	att	144
Phe	Val	Met	Asp	Tyr	Glu	Glu	Gly	Ile	Gly	Trp	His	His	Pro	Arg	Ile	
		35					40					45				
gcg	ccg	tac	gca	ccg	ctt	acg	ctt	gat	ccg	tct	tca	tct	gtt	ttt	cat	192
Ala	Pro	Tyr	Ala	Pro	Leu	Thr	Leu	Asp	Pro	Ser	Ser	Ser	Val	Phe	His	
	50					55					60					
tac	ggc	cag	gct	gtt	ttt	gaa	gga	tta	aaa	gca	tac	aga	aca	gac	gac	240
Tyr	Gly	Gln	Ala	Val	Phe	Glu	Gly	Leu	Lys	Ala	Tyr	Arg	Thr	Asp	Asp	
65					70					75					80	
ggc	agg	gtg	ctg	ctg	ttc	cgt	ccg	gat	caa	aat	atc	aaa	cgg	ctg	aac	288
Gly	Arg	Val	Leu	Leu	Phe	Arg	Pro	Asp	Gln	Asn	Ile	Lys	Arg	Leu	Asn	
				85					90					95		
aga	tcg	tgt	gag	cgc	atg	agc	atg	ccc	cct	tta	gac	gaa	gag	ctg	gtg	336
Arg	Ser	Cys	Glu	Arg	Met	Ser	Met	Pro	Pro	Leu	Asp	Glu	Glu	Leu	Val	
			100					105					110			
ctt	gag	gca	ttg	acg	caa	tta	gtt	gag	ctg	gag	aaa	gat	tgg	gtt	cca	384
Leu	Glu	Ala	Leu	Thr	Gln	Leu	Val	Glu	Leu	Glu	Lys	Asp	Trp	Val	Pro	
		115					120					125				
aag	gaa	aaa	gga	acg	tca	ctg	tat	att	cgt	cct	ttt	gtc	att	gcc	aca	432
Lys	Glu	Lys	Gly	Thr	Ser	Leu	Tyr	Ile	Arg	Pro	Phe	Val	Ile	Ala	Thr	
	130					135					140					
gaa	ccg	agt	ctc	ggt	gtg	aag	gca	tcc	agg	agc	tat	aca	ttt	atg	atc	480

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Glu 145	Pro	Ser	Leu	Gly	Val 150	Lys	Ala	Ser	Arg	Ser 155	Tyr	Thr	Phe	Met	Ile 160	
gtg	ctt	tcg	cct	gtc	ggc	tcc	tat	tat	ggc	gac	gat	cag	ctg	aag	ccg	528
Val	Leu	Ser	Pro	Val	Gly	Ser	Tyr	Tyr	Gly	Asp	Asp	Gln	Leu	Lys	Pro	
				165					170					175		
ggt	aga	atc	tat	gtc	gaa	gat	gag	tat	gtg	agg	gcg	gtc	aac	gga	gga	576
Val	Arg	Ile	Tyr	Val	Glu	Asp	Glu	Tyr	Val	Arg	Ala	Val	Asn	Gly	Gly	
			180					185					190			
gtc	ggg	ttt	gca	aaa	acg	gct	gga	aac	tat	gcc	gcc	agt	ctt	cag	gca	624
Val	Gly	Phe	Ala	Lys	Thr	Ala	Gly	Asn	Tyr	Ala	Ala	Ser	Leu	Gln	Ala	
		195					200					205				
cag	cgg	aaa	gcg	aat	gaa	ctg	ggc	tat	gac	cag	gta	ctg	tgg	ctg	gac	672
Gln	Arg	Lys	Ala	Asn	Glu	Leu	Gly	Tyr	Asp	Gln	Val	Leu	Trp	Leu	Asp	
	210					215					220					
gcc	atc	gaa	aag	aaa	tat	gtg	gaa	gaa	gta	ggg	agc	atg	aac	atc	ttt	720
Ala	Ile	Glu	Lys	Lys	Tyr	Val	Glu	Glu	Val	Gly	Ser	Met	Asn	Ile	Phe	
225					230					235					240	
ttc	gtc	ata	aac	ggg	gaa	gct	gtc	aca	cct	gct	tta	agc	gga	agc	att	768
Phe	Val	Ile	Asn	Gly	Glu	Ala	Val	Thr	Pro	Ala	Leu	Ser	Gly	Ser	Ile	
				245					250					255		
tta	agc	ggg	gtt	aca	cgt	gcg	tct	gcg	att	gaa	ttg	att	cga	agc	tgg	816
Leu	Ser	Gly	Val	Thr	Arg	Ala	Ser	Ala	Ile	Glu	Leu	Ile	Arg	Ser	Trp	
			260					265					270			
ggc	att	ccg	gtt	cgt	gaa	gag	aga	ata	tcg	att	gat	gag	gtg	tat	gcg	864
Gly	Ile	Pro	Val	Arg	Glu	Glu	Arg	Ile	Ser	Ile	Asp	Glu	Val	Tyr	Ala	
		275					280					285				
gcc	tct	gca	cgc	gga	gaa	ttg	aca	gag	gtc	ttt	ggc	aca	ggc	acg	gca	912
Ala	Ser	Ala	Arg	Gly	Glu	Leu	Thr	Glu	Val	Phe	Gly	Thr	Gly	Thr	Ala	
290						295					300					
gca	gtc	gtt	acg	cct	gtc	ggt	gaa	ctc	aac	atc	cat	gga	aaa	acg	gtg	960
Ala	Val	Val	Thr	Pro	Val	Gly	Glu	Leu	Asn	Ile	His	Gly	Lys	Thr	Val	
305					310					315					320	
att	gta	ggc	gac	ggg	caa	atc	ggg	gac	ctc	tcg	aaa	aag	ctg	tat	gaa	1008
Ile	Val	Gly	Asp	Gly	Gln	Ile	Gly	Asp	Leu	Ser	Lys	Lys	Leu	Tyr	Glu	
				325					330					335		
acg	ata	aca	gat	att	cag	ctt	ggc	aag	gta	aaa	ggc	ccg	ttt	aac	tgg	1056
Thr	Ile	Thr	Asp	Ile	Gln	Leu	Gly	Lys	Val	Lys	Gly	Pro	Phe	Asn	Trp	
			340					345					350			
aca	gtg	gaa	gtg	tga												1071
Thr	Val	Glu	Val													
			355													

<210> 65

<211> 356

<212> PRT

<213> Bacillus subtilis

<400> 65

Met	Asn	Lys	Leu	Ile	Glu	Arg	Glu	Lys	Thr	Val	Tyr	Tyr	Lys	Glu	Lys	1	5	10	15
Pro	Asp	Pro	Ser	Ser	Leu	Gly	Phe	Gly	Gln	Tyr	Phe	Thr	Asp	Tyr	Met	20	25	30	
Phe	Val	Met	Asp	Tyr	Glu	Glu	Gly	Ile	Gly	Trp	His	His	Pro	Arg	Ile	35	40	45	
Ala	Pro	Tyr	Ala	Pro	Leu	Thr	Leu	Asp	Pro	Ser	Ser	Ser	Val	Phe	His	50	55	60	
Tyr	Gly	Gln	Ala	Val	Phe	Glu	Gly	Leu	Lys	Ala	Tyr	Arg	Thr	Asp	Asp	65	70	75	80
Gly	Arg	Val	Leu	Leu	Phe	Arg	Pro	Asp	Gln	Asn	Ile	Lys	Arg	Leu	Asn	85	90	95	
Arg	Ser	Cys	Glu	Arg	Met	Ser	Met	Pro	Pro	Leu	Asp	Glu	Glu	Leu	Val	100	105	110	
Leu	Glu	Ala	Leu	Thr	Gln	Leu	Val	Glu	Leu	Glu	Lys	Asp	Trp	Val	Pro	115	120	125	
Lys	Glu	Lys	Gly	Thr	Ser	Leu	Tyr	Ile	Arg	Pro	Phe	Val	Ile	Ala	Thr	130	135	140	
Glu	Pro	Ser	Leu	Gly	Val	Lys	Ala	Ser	Arg	Ser	Tyr	Thr	Phe	Met	Ile	145	150	155	160
Val	Leu	Ser	Pro	Val	Gly	Ser	Tyr	Tyr	Gly	Asp	Asp	Gln	Leu	Lys	Pro	165	170	175	
Val	Arg	Ile	Tyr	Val	Glu	Asp	Glu	Tyr	Val	Arg	Ala	Val	Asn	Gly	Gly	180	185	190	
Val	Gly	Phe	Ala	Lys	Thr	Ala	Gly	Asn	Tyr	Ala	Ala	Ser	Leu	Gln	Ala	195	200	205	
Gln	Arg	Lys	Ala	Asn	Glu	Leu	Gly	Tyr	Asp	Gln	Val	Leu	Trp	Leu	Asp	210	215	220	
Ala	Ile	Glu	Lys	Lys	Tyr	Val	Glu	Glu	Val	Gly	Ser	Met	Asn	Ile	Phe	225	230	235	240
Phe	Val	Ile	Asn	Gly	Glu	Ala	Val	Thr	Pro	Ala	Leu	Ser	Gly	Ser	Ile	245	250	255	
Leu	Ser	Gly	Val	Thr	Arg	Ala	Ser	Ala	Ile	Glu	Leu	Ile	Arg	Ser	Trp	260	265	270	
Gly	Ile	Pro	Val	Arg	Glu	Glu	Arg	Ile	Ser	Ile	Asp	Glu	Val	Tyr	Ala	275	280	285	

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Ala Ser Ala Arg Gly Glu Leu Thr Glu Val Phe Gly Thr Gly Thr Ala
 290 295 300

Ala Val Val Thr Pro Val Gly Glu Leu Asn Ile His Gly Lys Thr Val
 305 310 315 320

Ile Val Gly Asp Gly Gln Ile Gly Asp Leu Ser Lys Lys Leu Tyr Glu
 325 330 335

Thr Ile Thr Asp Ile Gln Leu Gly Lys Val Lys Gly Pro Phe Asn Trp
 340 345 350

Thr Val Glu Val
 355

<210> 66

<211> 1428

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(1425)

<400> 66

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gaa aaa caa att gaa gca gat gtt tat tac gga att cag acg ctc cgt	96
Glu Lys Gln Ile Glu Ala Asp Val Tyr Tyr Gly Ile Gln Thr Leu Arg	
20 25 30	
gct tct gaa aat ttt ccg atc aca gga tac aaa atc cat gag gaa atg	144
Ala Ser Glu Asn Phe Pro Ile Thr Gly Tyr Lys Ile His Glu Glu Met	
35 40 45	
att aac gca ctg gcg att gtg aaa aaa gct gcg gct ctt gcc aac atg	192
Ile Asn Ala Leu Ala Ile Val Lys Lys Ala Ala Ala Leu Ala Asn Met	
50 55 60	
gac gtg aaa cgg ctg tat gaa gga att ggc caa gct atc gta caa gcc	240
Asp Val Lys Arg Leu Tyr Glu Gly Ile Gly Gln Ala Ile Val Gln Ala	
65 70 75 80	
gct gac gag att ctg gaa ggc aag tgg cac gat cag ttt atc gtc gat	288
Ala Asp Glu Ile Leu Glu Gly Lys Trp His Asp Gln Phe Ile Val Asp	
85 90 95	
ccg att cag ggc ggt gcc gga act tct atg aac atg aac gcg aat gag	336
Pro Ile Gln Gly Gly Ala Gly Thr Ser Met Asn Met Asn Ala Asn Glu	
100 105 110	
gtt atc gga aac cgg gcg ctt gaa atc atg gga cat aaa aag gga gat	384
Val Ile Gly Asn Arg Ala Leu Glu Ile Met Gly His Lys Lys Gly Asp	
115 120 125	

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tat	atc	cat	tta	agt	cca	aac	aca	cat	gtg	aac	atg	tca	cag	tct	cag	432
Tyr	Ile	His	Leu	Ser	Pro	Asn	Thr	His	Val	Asn	Met	Ser	Gln	Ser	Gln	
130						135					140					
aac	gat	gtg	ttc	ccg	act	gct	atc	cat	att	tcc	aca	ttg	aag	ctc	tta	480
Asn	Asp	Val	Phe	Pro	Thr	Ala	Ile	His	Ile	Ser	Thr	Leu	Lys	Leu	Leu	
145					150					155					160	
gaa	aaa	ctg	ctg	aaa	aca	atg	gaa	gat	atg	cat	agt	gtg	ttt	aaa	caa	528
Glu	Lys	Leu	Leu	Lys	Thr	Met	Glu	Asp	Met	His	Ser	Val	Phe	Lys	Gln	
				165					170					175		
aaa	gca	cag	gag	ttt	cac	tct	gtt	att	aaa	atg	ggc	cgg	aca	cac	ctt	576
Lys	Ala	Gln	Glu	Phe	His	Ser	Val	Ile	Lys	Met	Gly	Arg	Thr	His	Leu	
			180					185					190			
caa	gat	gcg	gtt	ccg	atc	cgt	ctt	ggc	cag	gaa	ttc	gaa	gct	tac	agc	624
Gln	Asp	Ala	Val	Pro	Ile	Arg	Leu	Gly	Gln	Glu	Phe	Glu	Ala	Tyr	Ser	
		195					200					205				
cgt	gtt	ctc	gag	cgt	gat	atc	aaa	cga	atc	aag	caa	tcg	cgc	cag	cac	672
Arg	Val	Leu	Glu	Arg	Asp	Ile	Lys	Arg	Ile	Lys	Gln	Ser	Arg	Gln	His	
	210					215					220					
ctg	tat	gaa	gtc	aac	atg	ggc	gca	act	gct	gtt	ggg	aca	ggg	ctg	aac	720
Leu	Tyr	Glu	Val	Asn	Met	Gly	Ala	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	
225					230					235					240	
gct	gat	cct	gaa	tat	atc	aaa	cag	gta	gta	aag	cac	ctt	gct	gat	att	768
Ala	Asp	Pro	Glu	Tyr	Ile	Lys	Gln	Val	Val	Lys	His	Leu	Ala	Asp	Ile	
				245				250						255		
agc	ggg	ctt	cct	ctt	gtc	ggc	gct	gat	cat	ctt	gtt	gat	gcg	aca	caa	816
Ser	Gly	Leu	Pro	Leu	Val	Gly	Ala	Asp	His	Leu	Val	Asp	Ala	Thr	Gln	
			260					265					270			
aat	aca	gat	gcc	tat	aca	gag	gta	tca	gct	tca	tta	aaa	gtc	tgc	atg	864
Asn	Thr	Asp	Ala	Tyr	Thr	Glu	Val	Ser	Ala	Ser	Leu	Lys	Val	Cys	Met	
		275					280					285				
atg	aac	atg	tcg	aag	atc	gca	aac	gac	ctg	cgc	tta	atg	gcg	tcg	gga	912
Met	Asn	Met	Ser	Lys	Ile	Ala	Asn	Asp	Leu	Arg	Leu	Met	Ala	Ser	Gly	
	290					295					300					
ccg	cgc	gcc	gga	ctt	gcg	gaa	att	tct	ctg	cct	gca	cgt	cag	ccg	ggt	960
Pro	Arg	Ala	Gly	Leu	Ala	Glu	Ile	Ser	Leu	Pro	Ala	Arg	Gln	Pro	Gly	
305					310					315					320	
tca	tct	att	atg	ccg	ggg	aaa	gtc	aat	ccg	gtt	atg	gcg	gag	ctg	atc	1008
Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Met	Ala	Glu	Leu	Ile	
				325					330					335		
aac	caa	att	gcg	ttc	cag	gtt	atc	gga	aat	gac	aat	aca	atc	tgc	ctt	1056
Asn	Gln	Ile	Ala	Phe	Gln	Val	Ile	Gly	Asn	Asp	Asn	Thr	Ile	Cys	Leu	
			340					345					350			
gct	tca	gaa	gcc	ggc	cag	ctt	gag	ttg	aac	gtc	atg	gag	ccc	gtg	ctt	1104
Ala	Ser	Glu	Ala	Gly	Gln	Leu	Glu	Leu	Asn	Val	Met	Glu	Pro	Val	Leu	

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355						360						365						
gtc	ttt	aat	ttg	ctt	caa	tcc	atc	agc	atc	atg	aac	aac	ggc	ttc	cgt	1152		
Val	Phe	Asn	Leu	Leu	Gln	Ser	Ile	Ser	Ile	Met	Asn	Asn	Gly	Phe	Arg			
370						375						380						
tcg	ttc	act	gac	aac	tgc	tta	aaa	ggc	att	gaa	gcc	aac	gaa	aag	cgt	1200		
Ser	Phe	Thr	Asp	Asn	Cys	Leu	Lys	Gly	Ile	Glu	Ala	Asn	Glu	Lys	Arg			
385						390						395						400
atg	aag	caa	tac	gta	gaa	aaa	agc	gca	ggc	gtg	atc	aca	gct	gtc	aat	1248		
Met	Lys	Gln	Tyr	Val	Glu	Lys	Ser	Ala	Gly	Val	Ile	Thr	Ala	Val	Asn			
405						410						415						
ccg	cat	ctt	ggg	tat	gaa	gcg	gca	gct	aga	att	gcc	agg	gaa	gca	att	1296		
Pro	His	Leu	Gly	Tyr	Glu	Ala	Ala	Ala	Arg	Ile	Ala	Arg	Glu	Ala	Ile			
420						425						430						
atg	aca	ggg	caa	tct	gtc	cgg	gat	ctt	tgt	ctg	cag	cat	gat	gtg	ctg	1344		
Met	Thr	Gly	Gln	Ser	Val	Arg	Asp	Leu	Cys	Leu	Gln	His	Asp	Val	Leu			
435						440						445						
act	gaa	gaa	gaa	ttg	gat	att	att	tta	aac	cca	tat	gag	atg	acc	aaa	1392		
Thr	Glu	Glu	Glu	Leu	Asp	Ile	Ile	Leu	Asn	Pro	Tyr	Glu	Met	Thr	Lys			
450						455						460						
cca	ggt	atc	gca	ggg	aaa	gaa	cta	tta	gaa	aaa	taa					1428		
Pro	Gly	Ile	Ala	Gly	Lys	Glu	Leu	Leu	Glu	Lys								
465						470						475						

<210> 67

<211> 475

<212> PRT

<213> Bacillus subtilis

<400> 67

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Glu	Lys	Gln	Ile	Glu	Ala	Asp	Val	Tyr	Tyr	Gly	Ile	Gln	Thr	Leu	Arg
		20					25					30			

Ala	Ser	Glu	Asn	Phe	Pro	Ile	Thr	Gly	Tyr	Lys	Ile	His	Glu	Glu	Met
		35				40					45				

Ile	Asn	Ala	Leu	Ala	Ile	Val	Lys	Lys	Ala	Ala	Ala	Leu	Ala	Asn	Met
	50				55				60						

Asp	Val	Lys	Arg	Leu	Tyr	Glu	Gly	Ile	Gly	Gln	Ala	Ile	Val	Gln	Ala
65				70				75						80	

Ala	Asp	Glu	Ile	Leu	Glu	Gly	Lys	Trp	His	Asp	Gln	Phe	Ile	Val	Asp
		85					90						95		

Pro	Ile	Gln	Gly	Gly	Ala	Gly	Thr	Ser	Met	Asn	Met	Asn	Ala	Asn	Glu
		100					105					110			

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Val	Ile	Gly	Asn	Arg	Ala	Leu	Glu	Ile	Met	Gly	His	Lys	Lys	Gly	Asp	115	120	125
Tyr	Ile	His	Leu	Ser	Pro	Asn	Thr	His	Val	Asn	Met	Ser	Gln	Ser	Gln	130	135	140
Asn	Asp	Val	Phe	Pro	Thr	Ala	Ile	His	Ile	Ser	Thr	Leu	Lys	Leu	Leu	145	150	155
Glu	Lys	Leu	Leu	Lys	Thr	Met	Glu	Asp	Met	His	Ser	Val	Phe	Lys	Gln	165	170	175
Lys	Ala	Gln	Glu	Phe	His	Ser	Val	Ile	Lys	Met	Gly	Arg	Thr	His	Leu	180	185	190
Gln	Asp	Ala	Val	Pro	Ile	Arg	Leu	Gly	Gln	Glu	Phe	Glu	Ala	Tyr	Ser	195	200	205
Arg	Val	Leu	Glu	Arg	Asp	Ile	Lys	Arg	Ile	Lys	Gln	Ser	Arg	Gln	His	210	215	220
Leu	Tyr	Glu	Val	Asn	Met	Gly	Ala	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	225	230	235
Ala	Asp	Pro	Glu	Tyr	Ile	Lys	Gln	Val	Val	Lys	His	Leu	Ala	Asp	Ile	245	250	255
Ser	Gly	Leu	Pro	Leu	Val	Gly	Ala	Asp	His	Leu	Val	Asp	Ala	Thr	Gln	260	265	270
Asn	Thr	Asp	Ala	Tyr	Thr	Glu	Val	Ser	Ala	Ser	Leu	Lys	Val	Cys	Met	275	280	285
Met	Asn	Met	Ser	Lys	Ile	Ala	Asn	Asp	Leu	Arg	Leu	Met	Ala	Ser	Gly	290	295	300
Pro	Arg	Ala	Gly	Leu	Ala	Glu	Ile	Ser	Leu	Pro	Ala	Arg	Gln	Pro	Gly	305	310	315
Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Met	Ala	Glu	Leu	Ile	325	330	335
Asn	Gln	Ile	Ala	Phe	Gln	Val	Ile	Gly	Asn	Asp	Asn	Thr	Ile	Cys	Leu	340	345	350
Ala	Ser	Glu	Ala	Gly	Gln	Leu	Glu	Leu	Asn	Val	Met	Glu	Pro	Val	Leu	355	360	365
Val	Phe	Asn	Leu	Leu	Gln	Ser	Ile	Ser	Ile	Met	Asn	Asn	Gly	Phe	Arg	370	375	380
Ser	Phe	Thr	Asp	Asn	Cys	Leu	Lys	Gly	Ile	Glu	Ala	Asn	Glu	Lys	Arg	385	390	395
Met	Lys	Gln	Tyr	Val	Glu	Lys	Ser	Ala	Gly	Val	Ile	Thr	Ala	Val	Asn	405	410	415
Pro	His	Leu	Gly	Tyr	Glu	Ala	Ala	Ala	Arg	Ile	Ala	Arg	Glu	Ala	Ile			

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420 425 430
 Met Thr Gly Gln Ser Val Arg Asp Leu Cys Leu Gln His Asp Val Leu
 435 440 445
 Thr Glu Glu Glu Leu Asp Ile Ile Leu Asn Pro Tyr Glu Met Thr Lys
 450 455 460
 Pro Gly Ile Ala Gly Lys Glu Leu Leu Glu Lys
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<210> 68

<211> 768

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1) .. (765)

<400> 68

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 Met Lys Arg Glu Ser Asn Ile Gln Val Leu Ser Arg Gly Gln Lys Asp
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cag cct gtg agc cag att tat caa gta tca aca atg act tct cta tta 96
 Gln Pro Val Ser Gln Ile Tyr Gln Val Ser Thr Met Thr Ser Leu Leu
 20 25 30

gac gga gta tat gac gga gat ttt gaa ctg tca gag att ccg aaa tat 144
 Asp Gly Val Tyr Asp Gly Asp Phe Glu Leu Ser Glu Ile Pro Lys Tyr
 35 40 45

gga gac ttc ggt atc gga acc ttt aac aag ctt gac gga gag ctg att 192
 Gly Asp Phe Gly Ile Gly Thr Phe Asn Lys Leu Asp Gly Glu Leu Ile
 50 55 60

ggg ttt gac ggc gaa ttt tac cgt ctt cgc tca gac gga acc gcg aca 240
 Gly Phe Asp Gly Glu Phe Tyr Arg Leu Arg Ser Asp Gly Thr Ala Thr
 65 70 75 80

ccg gtc caa aat gga gac cgt tca ccg ttc tgt tca ttt acg ttc ttt 288
 Pro Val Gln Asn Gly Asp Arg Ser Pro Phe Cys Ser Phe Thr Phe Phe
 85 90 95

aca ccg gac atg acg cac aaa att gat gcg aaa atg aca cgc gaa gac 336
 Thr Pro Asp Met Thr His Lys Ile Asp Ala Lys Met Thr Arg Glu Asp
 100 105 110

ttt gaa aaa gag atc aac agc atg ctg cca agc aga aac tta ttt tat 384
 Phe Glu Lys Glu Ile Asn Ser Met Leu Pro Ser Arg Asn Leu Phe Tyr
 115 120 125

gca att cgc att gac gga ttg ttt aaa aag gtg cag aca aga aca gta 432
 Ala Ile Arg Ile Asp Gly Leu Phe Lys Lys Val Gln Thr Arg Thr Val
 130 135 140

- 72 -

gaa ctt caa gaa aaa cct tac gtg cca atg gtt gaa gcg gtc aaa aca 480
 Glu Leu Gln Glu Lys Pro Tyr Val Pro Met Val Glu Ala Val Lys Thr
 145 150 155 160

cag ccg att ttc aac ttc gac aac gtg aga gga acg att gta ggt ttc 528
 Gln Pro Ile Phe Asn Phe Asp Asn Val Arg Gly Thr Ile Val Gly Phe
 165 170 175

ttg aca cca gct tat gca aac gga atc gcc gtt tct ggc tat cac ctg 576
 Leu Thr Pro Ala Tyr Ala Asn Gly Ile Ala Val Ser Gly Tyr His Leu
 180 185 190

cac ttc att gac gaa gga cgc aat tca ggc gga cac gtt ttt gac tat 624
 His Phe Ile Asp Glu Gly Arg Asn Ser Gly Gly His Val Phe Asp Tyr
 195 200 205

gtg ctt gag gat tgc acg gtt acg att tct caa aaa atg aac atg aat 672
 Val Leu Glu Asp Cys Thr Val Thr Ile Ser Gln Lys Met Asn Met Asn
 210 215 220

ctc aga ctt ccg aac aca gcg gat ttc ttt aat gcg aat ctg gat aac 720
 Leu Arg Leu Pro Asn Thr Ala Asp Phe Phe Asn Ala Asn Leu Asp Asn
 225 230 235 240

cct gat ttt gcg aaa gat atc gaa aca act gaa gga agc cct gaa taa 768
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 245 250 255

<210> 69

<211> 255

<212> PRT

<213> Bacillus subtilis

<400> 69

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Gln Pro Val Ser Gln Ile Tyr Gln Val Ser Thr Met Thr Ser Leu Leu
 20 25 30

Asp Gly Val Tyr Asp Gly Asp Phe Glu Leu Ser Glu Ile Pro Lys Tyr
 35 40 45

Gly Asp Phe Gly Ile Gly Thr Phe Asn Lys Leu Asp Gly Glu Leu Ile
 50 55 60

Gly Phe Asp Gly Glu Phe Tyr Arg Leu Arg Ser Asp Gly Thr Ala Thr
 65 70 75 80

Pro Val Gln Asn Gly Asp Arg Ser Pro Phe Cys Ser Phe Thr Phe Phe
 85 90 95

Thr Pro Asp Met Thr His Lys Ile Asp Ala Lys Met Thr Arg Glu Asp
 100 105 110

Phe Glu Lys Glu Ile Asn Ser Met Leu Pro Ser Arg Asn Leu Phe Tyr
 115 120 125

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Ala	Ile	Arg	Ile	Asp	Gly	Leu	Phe	Lys	Lys	Val	Gln	Thr	Arg	Thr	Val
130						135					140				
Glu	Leu	Gln	Glu	Lys	Pro	Tyr	Val	Pro	Met	Val	Glu	Ala	Val	Lys	Thr
145					150					155					160
Gln	Pro	Ile	Phe	Asn	Phe	Asp	Asn	Val	Arg	Gly	Thr	Ile	Val	Gly	Phe
				165					170					175	
Leu	Thr	Pro	Ala	Tyr	Ala	Asn	Gly	Ile	Ala	Val	Ser	Gly	Tyr	His	Leu
			180					185					190		
His	Phe	Ile	Asp	Glu	Gly	Arg	Asn	Ser	Gly	Gly	His	Val	Phe	Asp	Tyr
		195					200					205			
Val	Leu	Glu	Asp	Cys	Thr	Val	Thr	Ile	Ser	Gln	Lys	Met	Asn	Met	Asn
210						215					220				
Leu	Arg	Leu	Pro	Asn	Thr	Ala	Asp	Phe	Phe	Asn	Ala	Asn	Leu	Asp	Asn
225					230					235					240
Pro	Asp	Phe	Ala	Lys	Asp	Ile	Glu	Thr	Thr	Glu	Gly	Ser	Pro	Glu	
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<211> 1254

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(1251)

<400> 70

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Met	Thr	Phe	Ser	Leu	Phe	Gly	Asp	Lys	Phe	Thr	Arg	His	Ser	Gly	Ile	
1				5					10					15		
acg	ctg	ttg	atg	gaa	gat	ctg	aac	gac	ggt	tta	cgc	acg	cct	ggc	gcg	96
Thr	Leu	Leu	Met	Glu	Asp	Leu	Asn	Asp	Gly	Leu	Arg	Thr	Pro	Gly	Ala	
			20					25					30			
att	atg	ctc	ggc	ggc	ggt	aat	ccg	gcg	cag	atc	ccg	gaa	atg	cag	gac	144
Ile	Met	Leu	Gly	Gly	Gly	Asn	Pro	Ala	Gln	Ile	Pro	Glu	Met	Gln	Asp	
		35				40					45					
tac	ttc	cag	acg	cta	ctg	acc	gac	atg	ctg	gaa	agt	ggc	aaa	gcg	act	192
Tyr	Phe	Gln	Thr	Leu	Leu	Thr	Asp	Met	Leu	Glu	Ser	Gly	Lys	Ala	Thr	
		50				55				60						
gat	gca	ctg	tgt	aac	tac	gac	ggt	cca	cag	ggg	aaa	acg	gag	cta	ctc	240
Asp	Ala	Leu	Cys	Asn	Tyr	Asp	Gly	Pro	Gln	Gly	Lys	Thr	Glu	Leu	Leu	
65				70					75					80		
aca	ctg	ctt	gcc	gga	atg	ctg	cgc	gag	aag	ttg	ggt	tgg	gat	atc	gaa	288
Thr	Leu	Leu	Ala	Gly	Met	Leu	Arg	Glu	Lys	Leu	Gly	Trp	Asp	Ile	Glu	

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85								90					95				
cca	cag	aat	att	gca	cta	aca	aac	ggc	agc	cag	agc	gcg	ttt	ttc	tac	336	
Pro	Gln	Asn	Ile	Ala	Leu	Thr	Asn	Gly	Ser	Gln	Ser	Ala	Phe	Phe	Tyr		
			100					105					110				
tta	ttt	aac	ctg	ttt	gcc	gga	cgc	cgt	gcc	gat	ggt	cgg	gtc	aaa	aaa	384	
Leu	Phe	Asn	Leu	Phe	Ala	Gly	Arg	Arg	Ala	Asp	Gly	Arg	Val	Lys	Lys		
		115					120					125					
gtg	ctg	ttc	ccg	ctt	gca	ccg	gaa	tac	att	ggc	tat	gct	gac	gcc	gga	432	
Val	Leu	Phe	Pro	Leu	Ala	Pro	Glu	Tyr	Ile	Gly	Tyr	Ala	Asp	Ala	Gly		
	130					135					140						
ctg	gaa	gaa	gat	ctg	ttt	gtc	tct	gcg	cgt	ccg	aat	att	gaa	ctg	ctg	480	
Leu	Glu	Glu	Asp	Leu	Phe	Val	Ser	Ala	Arg	Pro	Asn	Ile	Glu	Leu	Leu		
145					150					155					160		
ccg	gaa	ggc	cag	ttt	aaa	tac	cac	gtc	gat	ttt	gag	cat	ctg	cat	att	528	
Pro	Glu	Gly	Gln	Phe	Lys	Tyr	His	Val	Asp	Phe	Glu	His	Leu	His	Ile		
				165					170					175			
ggc	gaa	gaa	acc	ggg	atg	att	tgc	gtc	tcc	cgg	ccg	acg	aat	cca	aca	576	
Gly	Glu	Glu	Thr	Gly	Met	Ile	Cys	Val	Ser	Arg	Pro	Thr	Asn	Pro	Thr		
			180					185					190				
ggc	aat	gtg	att	act	gac	gaa	gag	ttg	ctg	aag	ctt	gac	gcg	ctg	ggc	624	
Gly	Asn	Val	Ile	Thr	Asp	Glu	Glu	Leu	Leu	Lys	Leu	Asp	Ala	Leu	Gly		
		195					200					205					
aat	caa	cac	ggc	att	ccg	ctg	gtg	att	gat	aac	gct	tat	ggc	gtc	ccg	672	
Asn	Gln	His	Gly	Ile	Pro	Leu	Val	Ile	Asp	Asn	Ala	Tyr	Gly	Val	Pro		
	210					215					220						
ttc	ccg	ggt	atc	atc	ttc	agt	gaa	gcg	cgc	ccg	cta	tgg	aat	ccg	aat	720	
Phe	Pro	Gly	Ile	Ile	Phe	Ser	Glu	Ala	Arg	Pro	Leu	Trp	Asn	Pro	Asn		
225					230					235					240		
atc	gtg	ctg	tgc	atg	agt	ctt	tcc	aag	ctg	ggt	cta	cct	ggc	tcc	cgc	768	
Ile	Val	Leu	Cys	Met	Ser	Leu	Ser	Lys	Leu	Gly	Leu	Pro	Gly	Ser	Arg		
				245					250					255			
tgc	ggc	att	atc	atc	gcc	aat	gaa	aaa	atc	atc	acc	gcc	atc	acc	aat	816	
Cys	Gly	Ile	Ile	Ile	Ala	Asn	Glu	Lys	Ile	Ile	Thr	Ala	Ile	Thr	Asn		
			260					265					270				
atg	aac	ggc	att	atc	agc	ctg	gca	cct	ggc	ggt	att	ggt	ccg	gcg	atg	864	
Met	Asn	Gly	Ile	Ile	Ser	Leu	Ala	Pro	Gly	Gly	Ile	Gly	Pro	Ala	Met		
		275					280					285					
atg	tgt	gaa	atg	att	aag	cgt	aac	gat	ctg	ctg	cgc	ctg	tct	gaa	aca	912	
Met	Cys	Glu	Met	Ile	Lys	Arg	Asn	Asp	Leu	Leu	Arg	Leu	Ser	Glu	Thr		
	290					295					300						
gtc	atc	aaa	ccg	ttt	tac	tac	cag	cgt	gtt	cag	gaa	act	atc	gcc	atc	960	
Val	Ile	Lys	Pro	Phe	Tyr	Tyr	Gln	Arg	Val	Gln	Glu	Thr	Ile	Ala	Ile		
305					310					315					320		

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att cgc cgc tat tta ccg gaa aat cgc tgc ctg att cat aaa ccg gaa	1008
Ile Arg Arg Tyr Leu Pro Glu Asn Arg Cys Leu Ile His Lys Pro Glu	
325 330 335	
gga gcc att ttc ctc tgg cta tgg ttt aag gat ttg ccc att acg acc	1056
Gly Ala Ile Phe Leu Trp Leu Trp Phe Lys Asp Leu Pro Ile Thr Thr	
340 345 350	
aag cag ctc tat cag cgc ctg aaa gca cgc ggc gtg ctg atg gtg ccg	1104
Lys Gln Leu Tyr Gln Arg Leu Lys Ala Arg Gly Val Leu Met Val Pro	
355 360 365	
ggg cac aac ttc ttc cca ggg ctg gat aaa ccg tgg ccg cat acg cat	1152
Gly His Asn Phe Phe Pro Gly Leu Asp Lys Pro Trp Pro His Thr His	
370 375 380	
caa tgt atg cgc atg aac tac gta cca gag ccg gag aaa att gag gcg	1200
Gln Cys Met Arg Met Asn Tyr Val Pro Glu Pro Glu Lys Ile Glu Ala	
385 390 395 400	
ggg gtg aag att ctg gcg gaa gag ata gaa aga gcc tgg gct gaa agt	1248
Gly Val Lys Ile Leu Ala Glu Glu Ile Glu Arg Ala Trp Ala Glu Ser	
405 410 415	
cac taa	1254
His	

<210> 71
 <211> 417
 <212> PRT
 <213> Escherichia coli

<400> 71
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His

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- 96 -

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Recombinant
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Recombinant
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<210> 83

<211> 4191

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant
 pAN263 plasmid

<400> 83

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gactgtaaaa agaaatcgaa aaagaccgtt ttgtgtgaaa acggtctttt tgtttccttt 660
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cggactgaac ggggggttcg tgcatacagt ccagcttgga gcgaactgcc taccgggaac 3960

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 cgaaaggcag gaacaggaga gcgcacgagg gagccgccag gggaaacgcc tggatatcttt 4080
 atagtcctgt cgggtttcgc caccactgat ttgagcgtca gatttcgtga tgcttgtcag 4140
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<211> 702

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(699)

<400> 84

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tat cat gat gga aaa tta gaa tat cac tgg cgt ata gaa aca agc agg 96
 Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg
 20 25 30

cat aaa aca gaa gat gag ttt ggg atg att ttg cgc tcc tta ttt gat 144
 His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Phe Asp
 35 40 45

cac tcc ggg ctt atg ttt gaa cag ata gat ggc att att att tcg tca 192
 His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser
 50 55 60

gta gtg ccg cca atc atg ttt gcg tta gaa aga atg tgc aca aaa tac 240
 Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Thr Lys Tyr
 65 70 75 80

ttt cat atc gag cct caa att gtt ggt cca ggt atg aaa acc ggt tta 288
 Phe His Ile Glu Pro Gln Ile Val Gly Pro Gly Met Lys Thr Gly Leu
 85 90 95

aat ata aaa tat gac aat ccg aaa gaa gta ggg gca gac aga atc gta 336
 Asn Ile Lys Tyr Asp Asn Pro Lys Glu Val Gly Ala Asp Arg Ile Val
 100 105 110

aat gct gtc gct gcg ata cac ttg tac ggc aat cca tta att gtt gtc 384
 Asn Ala Val Ala Ala Ile His Leu Tyr Gly Asn Pro Leu Ile Val Val
 115 120 125

gat ttc gga acc gcc aca acg tac tgc tat att gat gaa aac aaa caa 432
 Asp Phe Gly Thr Ala Thr Thr Tyr Cys Tyr Ile Asp Glu Asn Lys Gln
 130 135 140

tac atg ggc ggg gcg att gcc cct ggg att aca att tcg aca gag gcg 480
 Tyr Met Gly Gly Ala Ile Ala Pro Gly Ile Thr Ile Ser Thr Glu Ala
 145 150 155 160

cgc tca ttg cga acg aat cag att gta tag 702
Arg Ser Leu Arg Thr Asn Gln Ile Val
225 230

<213> Bacillus subtilis

Tyr Met Gly Gly Ala Ile Ala Pro Gly Ile Thr Ile Ser Thr Glu Ala
145 150 155 160

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 165 170 175
 Asp Asn Ile Ile Gly Lys Asn Thr Val Ser Ala Met Gln Ser Gly Ile
 180 185 190
 Leu Phe Gly Tyr Val Gly Gln Val Glu Gly Ile Val Lys Arg Met Lys
 195 200 205
 Trp Gln Ala Lys Gln Asp Pro Arg Ser Leu Arg Gln Glu Ala Trp Arg
 210 215 220
 Arg Ser Leu Arg Thr Asn Gln Ile Val
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<210> 86

<211> 1623

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

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 tac aag ata aag gac ctg aaa tta tcg ttg ccc ggc acg aac aaa acg 96
 Tyr Lys Ile Lys Asp Leu Lys Leu Ser Leu Pro Gly Thr Asn Lys Thr
 20 25 30
 cag caa ttc atg gcc caa gca gtc ggc cgt tta act gga aaa ccg gga 144
 Gln Gln Phe Met Ala Gln Ala Val Gly Arg Leu Thr Gly Lys Pro Gly
 35 40 45
 gtc gtg tta gtc aca tca gga ccg ggt gcc tct aac ttg gca aca ggc 192
 Val Val Leu Val Thr Ser Gly Pro Gly Ala Ser Asn Leu Ala Thr Gly
 50 55 60
 ctg ctg aca gcg aac act gaa gga gac cct gtc gtt gcg ctt gct gga 240
 Leu Leu Thr Ala Asn Thr Glu Gly Asp Pro Val Val Ala Leu Ala Gly
 65 70 75 80
 aac gtg atc cgt gca tat cgt tta aaa cgg aca cat caa tct ttg gat 288
 Asn Val Ile Arg Ala Tyr Arg Leu Lys Arg Thr His Gln Ser Leu Asp
 85 90 95
 aat gcg gcg cta ttc cag ccg att aca aaa tac agt gta gaa gtt caa 336
 Asn Ala Ala Leu Phe Gln Pro Ile Thr Lys Tyr Ser Val Glu Val Gln
 100 105 110
 gat gta aaa aat ata ccg gaa gct gtt aca aat gca ttt agg ata gcg 384
 Asp Val Lys Asn Ile Pro Glu Ala Val Thr Asn Ala Phe Arg Ile Ala
 115 120 125
 tca gca ggg cag gct ggg gcc gct ttt gtg agc ttt ccg caa gat gtt 432

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Ser 130	Ala 130	Gly	Gln	Ala	Gly 135	Ala 135	Ala	Phe	Val	Ser	Phe 140	Pro	Gln	Asp	Val	
gtg	aat	gaa	gtc	aca	aat	acg	aaa	aac	gtg	cgt	gct	gtt	gca	gcg	cca	480
Val	Asn	Glu	Val	Thr	Asn	Thr	Lys	Asn	Val	Arg	Ala	Val	Ala	Ala	Pro	
145					150					155					160	
aaa	ctc	ggt	cct	gca	gca	gat	gat	gca	atc	agt	gcg	gcc	ata	gca	aaa	528
Lys	Leu	Gly	Pro	Ala	Ala	Asp	Asp	Ala	Ile	Ser	Ala	Ala	Ile	Ala	Lys	
				165					170					175		
atc	caa	aca	gca	aaa	ctt	cct	gtc	gtt	ttg	gtc	ggc	atg	aaa	ggc	gga	576
Ile	Gln	Thr	Ala	Lys	Leu	Pro	Val	Val	Leu	Val	Gly	Met	Lys	Gly	Gly	
			180					185					190			
aga	ccg	gaa	gca	att	aaa	gcg	gtt	cgc	aag	ctt	ttg	aaa	aag	gtt	cag	624
Arg	Pro	Glu	Ala	Ile	Lys	Ala	Val	Arg	Lys	Leu	Leu	Lys	Lys	Val	Gln	
		195					200					205				
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Leu	Pro	Phe	Val	Glu	Thr	Tyr	Gln	Ala	Ala	Gly	Thr	Leu	Ser	Arg	Asp	
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Gly	Asp	Leu	Leu	Leu	Glu	Gln	Ala	Asp	Val	Val	Leu	Thr	Ile	Gly	Tyr	
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gac	ccg	att	gaa	tat	gat	ccg	aaa	ttc	tgg	aat	atc	aat	gga	gac	cgg	816
Asp	Pro	Ile	Glu	Tyr	Asp	Pro	Lys	Phe	Trp	Asn	Ile	Asn	Gly	Asp	Arg	
			260					265					270			
aca	att	atc	cat	tta	gac	gag	att	atc	gct	gac	att	gat	cat	gct	tac	864
Thr	Ile	Ile	His	Leu	Asp	Glu	Ile	Ile	Ala	Asp	Ile	Asp	His	Ala	Tyr	
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cag	cct	gat	ctt	gaa	ttg	atc	ggt	gac	att	ccg	tcc	acg	atc	aat	cat	912
Gln	Pro	Asp	Leu	Glu	Leu	Ile	Gly	Asp	Ile	Pro	Ser	Thr	Ile	Asn	His	
	290					295					300					
atc	gaa	cac	gat	gct	gtg	aaa	gtg	gaa	ttt	gca	gag	cgt	gag	cag	aaa	960
Ile	Glu	His	Asp	Ala	Val	Lys	Val	Glu	Phe	Ala	Glu	Arg	Glu	Gln	Lys	
305					310					315					320	
atc	ctt	tct	gat	tta	aaa	caa	tat	atg	cat	gaa	ggt	gag	cag	gtg	cct	1008
Ile	Leu	Ser	Asp	Leu	Lys	Gln	Tyr	Met	His	Glu	Gly	Glu	Gln	Val	Pro	
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gca	gat	tgg	aaa	tca	gac	aga	gcg	cac	cct	ctt	gaa	atc	gtt	aaa	gag	1056
Ala	Asp	Trp	Lys	Ser	Asp	Arg	Ala	His	Pro	Leu	Glu	Ile	Val	Lys	Glu	
			340					345					350			
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Leu	Arg	Asn	Ala	Val	Asp	Asp	His	Val	Thr	Val	Thr	Cys	Asp	Ile	Gly	
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Ser	His	Ser	Ile	Trp	Met	Ser	Arg	Tyr	Phe	Arg	Ser	Tyr	Glu	Pro	Leu	
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Thr	Leu	Met	Ile	Ser	Asn	Gly	Met	Gln	Thr	Leu	Gly	Val	Ala	Leu	Pro	
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Trp	Ala	Ile	Gly	Ala	Ser	Leu	Val	Lys	Pro	Gly	Glu	Lys	Val	Val	Ser	
			405					410					415			
gtc	tct	ggg	gac	ggc	ggg	ttc	tta	ttc	tca	gca	atg	gaa	tta	gag	aca	1296
Val	Ser	Gly	Asp	Gly	Gly	Phe	Leu	Phe	Ser	Ala	Met	Glu	Leu	Glu	Thr	
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gca	gtt	cga	cta	aaa	gca	cca	att	gta	cac	att	gta	tgg	aac	gac	agc	1344
Ala	Val	Arg	Leu	Lys	Ala	Pro	Ile	Val	His	Ile	Val	Trp	Asn	Asp	Ser	
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465					470					475					480	
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Phe	Gly	Ala	Thr	Ala	Leu	Arg	Val	Glu	Ser	Pro	Asp	Gln	Leu	Ala	Asp	
				485				490					495			
gtt	ctg	cgt	caa	ggc	atg	aac	gct	gaa	ggg	cct	gtc	atc	atc	gat	gtc	1536
Val	Leu	Arg	Gln	Gly	Met	Asn	Ala	Glu	Gly	Pro	Val	Ile	Ile	Asp	Val	
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Pro	Val	Asp	Tyr	Ser	Asp	Asn	Ile	Asn	Leu	Ala	Ser	Asp	Lys	Leu	Pro	
		515					520					525				
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<211> 540

<212> PRT

<213> Bacillus subtilis

<400> 87

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			20					25					30		

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Gln	Gln	Phe	Met	Ala	Gln	Ala	Val	Gly	Arg	Leu	Thr	Gly	Lys	Pro	Gly
		35					40					45			
Val	Val	Leu	Val	Thr	Ser	Gly	Pro	Gly	Ala	Ser	Asn	Leu	Ala	Thr	Gly
	50					55					60				
Leu	Leu	Thr	Ala	Asn	Thr	Glu	Gly	Asp	Pro	Val	Val	Ala	Leu	Ala	Gly
65					70					75					80
Asn	Val	Ile	Arg	Ala	Tyr	Arg	Leu	Lys	Arg	Thr	His	Gln	Ser	Leu	Asp
				85					90					95	
Asn	Ala	Ala	Leu	Phe	Gln	Pro	Ile	Thr	Lys	Tyr	Ser	Val	Glu	Val	Gln
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Asp	Val	Lys	Asn	Ile	Pro	Glu	Ala	Val	Thr	Asn	Ala	Phe	Arg	Ile	Ala
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Ser	Ala	Gly	Gln	Ala	Gly	Ala	Ala	Phe	Val	Ser	Phe	Pro	Gln	Asp	Val
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Val	Asn	Glu	Val	Thr	Asn	Thr	Lys	Asn	Val	Arg	Ala	Val	Ala	Ala	Pro
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Lys	Leu	Gly	Pro	Ala	Ala	Asp	Asp	Ala	Ile	Ser	Ala	Ala	Ile	Ala	Lys
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Ile	Gln	Thr	Ala	Lys	Leu	Pro	Val	Val	Leu	Val	Gly	Met	Lys	Gly	Gly
			180					185					190		
Arg	Pro	Glu	Ala	Ile	Lys	Ala	Val	Arg	Lys	Leu	Leu	Lys	Lys	Val	Gln
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Leu	Pro	Phe	Val	Glu	Thr	Tyr	Gln	Ala	Ala	Gly	Thr	Leu	Ser	Arg	Asp
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Leu	Glu	Asp	Gln	Tyr	Phe	Gly	Arg	Ile	Gly	Leu	Phe	Arg	Asn	Gln	Pro
225					230					235					240
Gly	Asp	Leu	Leu	Leu	Glu	Gln	Ala	Asp	Val	Val	Leu	Thr	Ile	Gly	Tyr
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Thr	Ile	Ile	His	Leu	Asp	Glu	Ile	Ile	Ala	Asp	Ile	Asp	His	Ala	Tyr
		275					280					285			
Gln	Pro	Asp	Leu	Glu	Leu	Ile	Gly	Asp	Ile	Pro	Ser	Thr	Ile	Asn	His
	290					295					300				
Ile	Glu	His	Asp	Ala	Val	Lys	Val	Glu	Phe	Ala	Glu	Arg	Glu	Gln	Lys
305					310					315					320
Ile	Leu	Ser	Asp	Leu	Lys	Gln	Tyr	Met	His	Glu	Gly	Glu	Gln	Val	Pro
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Ala	Asp	Trp	Lys	Ser	Asp	Arg	Ala	His	Pro	Leu	Glu	Ile	Val	Lys	Glu

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340								345				350			
Leu	Arg	Asn	Ala	Val	Asp	Asp	His	Val	Thr	Val	Thr	Cys	Asp	Ile	Gly
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Ser	His	Ser	Ile	Trp	Met	Ser	Arg	Tyr	Phe	Arg	Ser	Tyr	Glu	Pro	Leu
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Thr	Leu	Met	Ile	Ser	Asn	Gly	Met	Gln	Thr	Leu	Gly	Val	Ala	Leu	Pro
385					390					395					400
Trp	Ala	Ile	Gly	Ala	Ser	Leu	Val	Lys	Pro	Gly	Glu	Lys	Val	Val	Ser
				405					410					415	
Val	Ser	Gly	Asp	Gly	Gly	Phe	Leu	Phe	Ser	Ala	Met	Glu	Leu	Glu	Thr
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Ala	Val	Arg	Leu	Lys	Ala	Pro	Ile	Val	His	Ile	Val	Trp	Asn	Asp	Ser
		435					440					445			
Thr	Tyr	Asp	Met	Val	His	Phe	Gln	Gln	Leu	Lys	Lys	Tyr	Asn	Arg	Thr
	450					455					460				
Ser	Ala	Val	Asp	Phe	Gly	Asn	Ile	Asp	Ile	Val	Lys	Tyr	Ala	Glu	Ser
465					470					475					480
Phe	Gly	Ala	Thr	Ala	Leu	Arg	Val	Glu	Ser	Pro	Asp	Gln	Leu	Ala	Asp
				485					490					495	
Val	Leu	Arg	Gln	Gly	Met	Asn	Ala	Glu	Gly	Pro	Val	Ile	Ile	Asp	Val
			500					505					510		
Pro	Val	Asp	Tyr	Ser	Asp	Asn	Ile	Asn	Leu	Ala	Ser	Asp	Lys	Leu	Pro
		515				520						525			
Lys	Glu	Phe	Gly	Glu	Leu	Met	Lys	Thr	Lys	Ala	Leu				
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<210> 88

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: ribosome binding site

<220>

<223> All occurrences of n indicate any nucleotide

<400> 88

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23

<210> 89

<211> 7

<212> PRT

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PanC
C terminus

<400> 89

Ile Arg Glu Met Glu Arg Ile
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<210> 90

<211> 5

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: PanC
C terminus

<400> 90

Ile Arg Glu Arg Arg
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<210> 91

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PanC
C terminus

<400> 91

Ile Arg Arg Lys Glu Val Asn
1 5

<210> 92

<211> 6688

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant
pAN336 plasmid

<400> 92

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ttaagttggg taacgccagg gttttcccag tcacgacgtt gtaaaacgac ggccagtga 180

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<211> 8503

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant
 pAN004 plasmid

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- 145 -

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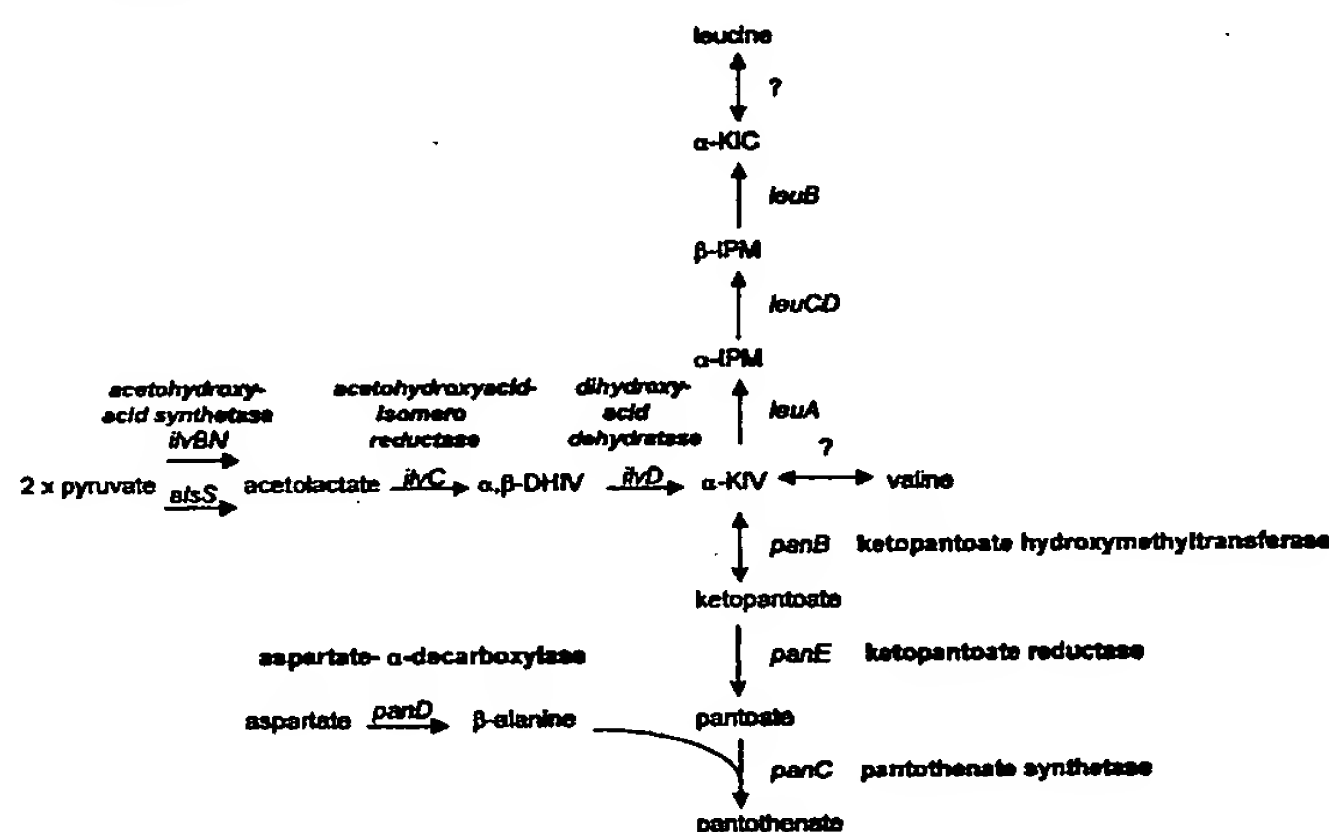
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For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.

(54) Title: METHODS AND MICROORGANISMS FOR PRODUCTION OF PANTO-COMPOUNDS



(57) Abstract: The present invention features methods of producing panto-compounds (<i>e.g.</i>, pantothenate) using microor-
ganisms in which the pantothenate biosynthetic pathway and/or the isoleucine-valine biosynthetic pathway and/or the coenzymeA
biosynthetic pathway has been manipulated. Methods featuring ketopantoate reductase overexpressing microorganisms as well as
aspartate g(a)-decarboxylase overexpressing microorganisms are provided. Methods of producing panto-compounds in a precur-
sor-independent manner and in high yield are described. Recombinant microorganisms, vectors, isolated nucleic acid molecules,
genes and gene products useful in practicing the above methodologies are also provided. The present invention also features a previ-
ously microbial pantothenate kinase gene, <i>coaX</i>, as well as methods of producing panto-compounds utilizing microorganisms
having modified pantothenate kinase activity. Recombinant microorganisms, vectors, isolated <i>coaX</i> nucleic acid molecules
and purified CoaX proteins are featured. Also featured are methods for identifying pantothenate kinase modulators utilizing the
recombinant microorganisms and/or purified CoaX proteins of the present invention.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/25993

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/52 C12N15/53 C12N15/54 C12N15/60 C12N15/75
C12N9/00 C12N9/02 C12N9/10 C12N9/12 C12N9/88
C12P7/42 C12P13/02 C12P13/06

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C12P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EMBL, EPO-Internal, WPI Data, PAJ, BIOSIS, MEDLINE, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP 0 590 857 A (TAKEDA CHEMICAL INDUSTRIES LTD) 6 April 1994 (1994-04-06) cited in the application	12,13, 24,26, 27,48, 51,55, 59,60, 71,76
Y	the whole document	1-6, 33-35, 54, 56-58, 62-64, 78-82
	page 14, line 1-3 --- -/--	

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☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

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Date of mailing of the international search report

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Name and mailing address of the ISA

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Int ional Application No
PCT/US 00/25993

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	SAHM H ET AL.: "D-Pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction" APPLIED AND ENVIRONMENTAL MICROBIOLOGY, vol. 65, no. 5, May 1999 (1999-05), pages 1973-1979, XP002169517 cited in the application	12,13, 24,26, 27,48, 51,54, 56,59, 60,71, 76,78,79
Y	the whole document	1-6, 33-35, 54, 56-58, 62-64, 78-82
X	--- SOROKIN A ET AL.: "Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial chromosome" MICROBIOLOGY, vol. 142, no. 8, 1996, pages 2005-2016, XP000910121 ISSN: 1350-0872	83-86, 92,93, 95, 97-100, 102,103
Y	abstract	1-6, 33-35, 54, 56-58, 62-64, 78-82
	page 2011, right-hand column, line 14-20; table 1	
X	--- DATABASE EM_PRO [Online] EMBL; ID BSYPIA, AC L47709, 23 January 1996 (1996-01-23) HENNER D ET AL.: "Bacillus subtilis (clone YAC15-6B) ypiABF genes, qcrABC genes, ypjABCDEFGHI genes, birA gene, panBCD genes, ding gene, ypmB gene, aspB gene, asnS gene, dnaD gene, nth gene and ypoC gene, complete cds." XP002171539 page 5, line 43-60 page 10	83-86, 98-100, 102,103
A	--- BAIGORI M ET AL.: "Isolation and characterization of Bacillus subtilis mutants blocked in the syntehsis of pantothenic acid" JOURNAL OF BACTERIOLOGY, vol. 173, no. 13, July 1991 (1991-07), pages 4240-4242, XP001002216 abstract	99,100, 102,103

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INTERNATIONAL SEARCH REPORT

In ational Application No

PCT/US 00/25993

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 98 18954 A (MONSANTO CO) 7 May 1998 (1998-05-07) the whole document ---	
A	EP 0 224 294 A (GIST BROCADES NV) 3 June 1987 (1987-06-03) the whole document ---	
P,X	EP 1 006 192 A (DEGUSSA) 7 June 2000 (2000-06-07) examples 2-5 ---	12,13, 24,26, 27,48, 51, 54-56, 59,60, 71,76, 78,79
P,X	EP 1 006 189 A (DEGUSSA ;KERNFORSCHUNGSANLAGE JUELICH (DE)) 7 June 2000 (2000-06-07) examples 1,7,9 -----	12,13, 24,26, 27,48, 51,54, 56,59, 60,71, 76,78,79

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Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-6,12,13,24,26-28,33-35,48,51,54-64,71,76,78-86,92,93,95,97,100,102,103
(all Partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-6,12,13,24,26-28,33-35,48,51,54-64,71,76,78-86, 92,93,95,97-100,102,103 (all partially)

A method of producing pantothenate (e.g., 2 g/L up to 40 g/L at least), pantoate, or ketopantoate, e.g., in a manner independent of precursor feed, comprising culturing a microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*) or Gram-negative) which overexpresses a ketopantoate hydroxymethyltransferase-encoding gene, e.g. the *panB* gene, e.g., from *Bacillus*, under conditions such that said panto-compound is produced, and possibly further recovering the compound. A recombinant microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus* (e.g., *Bacillus subtilis*), *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*)) which overexpresses a *Bacillus* (*subtilis*) ketopantoate hydroxymethyltransferase-encoding gene. A recombinant vector encoding a *Bacillus* (*subtilis*) ketopantoate hydroxymethyltransferase-encoding gene operably linked to regulatory sequences, e.g., comprising a nucleic acid sequence according to SEQ ID NO:23 or part of SEQ ID NO:59. An isolated nucleic acid molecule encoding a *Bacillus* (*subtilis*) ketopantoate hydroxymethyltransferase, and said isolated ketopantoate hydroxymethyltransferase polypeptide.

2. Claims: 1-6,12,13,24,26-28,33-35,48,51,54-64,71,76,78-86, 92,93,95,97-100,102,103 (all partially)

A method of producing panthotenate (e.g., 2 g/L up to 40 g/L at least), pantoate, or ketopantoate, e.g., in a manner independent of precursor feed, comprising culturing a microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*) or Gram-negative) which overexpresses a pantothenate synthetase-encoding gene, e.g. the *panC* gene, e.g., from *Bacillus*, under conditions such that said panto-compound is produced, and possibly further recovering the compound. A recombinant microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus* (e.g., *Bacillus subtilis*), *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*)) which overexpresses a *Bacillus* (*subtilis*) pantothenate synthetase-encoding gene. A recombinant vector encoding a *Bacillus* (*subtilis*) pantothenate synthetase-encoding gene operably linked to regulatory sequences, e.g., comprising a nucleic acid sequence according to SEQ ID NO:25 or part of SEQ ID NO:59. An isolated nucleic acid molecule encoding a *Bacillus* (*subtilis*) pantothenate synthetase, and said isolated pantothenate synthetase polypeptide.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

3. Claims: 1-6,12-14,24,26-28,33-35,48,49,51,54-64,66,71,76,
78-86,92,93,95,97-100,102,103 (all partially); 15,
17,19,23,32,106,107 (both completely)

A method of producing pantothenate (e.g., 2 g/L up to 40 g/L at least), pantoate, or ketopantoate, e.g., independent of aspartate or beta-alanine feed, comprising culturing a microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*) or Gram-negative) which overexpresses an aspartate-alpha-decarboxylase-encoding gene, e.g., from *Bacillus*, e.g., the aspartate-alpha-decarboxylase-encoding *panD* gene from *Bacillus subtilis*, under conditions such that said panto-compound is produced, and possibly further recovering the compound. A recombinant microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus* (e.g., *Bacillus subtilis*), *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*)) which overexpresses a *Bacillus* (*subtilis*) aspartate-alpha-decarboxylase-encoding gene. A recombinant vector encoding a *Bacillus* (*subtilis*) aspartate-alpha-decarboxylase-encoding gene operably linked to regulatory sequences, e.g., comprising a nucleic acid sequence according to SEQ ID NO:27 or part of SEQ ID NO:59. An isolated nucleic acid molecule encoding a *Bacillus* (*subtilis*) aspartate-alpha-decarboxylase, and said isolated aspartate-alpha-decarboxylase polypeptide.

4. Claims: 1-6,24,26-28,33-35,48,49,51,54-64,71,76,78-87,92,
93,95,97-100,102,103 (all partially); 7-11,65,101,
104,105 (all completely)

A method of producing pantothenate (e.g., 2 g/L up to 40 g/L at least), pantoate, or ketopantoate, e.g., independent of precursor feed, comprising culturing a microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*) or Gram-negative) which overexpresses a ketopantoate reductase-encoding gene, e.g., from *Bacillus*, e.g., the ketopantoate reductase-encoding *panE1* gene from *Bacillus subtilis*, under conditions such that said panto-compound is produced, and possibly further recovering the compound. A recombinant microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus* (e.g., *Bacillus subtilis*), *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*)) which overexpresses a *Bacillus* (*subtilis*) ketopantoate reductase-encoding gene. A recombinant vector encoding a *Bacillus* (*subtilis*) ketopantoate reductase-encoding gene operably linked to regulatory sequences, e.g., comprising a nucleic acid sequence according to SEQ ID NO:29. An isolated nucleic acid molecule encoding a *Bacillus* (*subtilis*)

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

ketopantoate reductase, and said isolated ketopantoate reductase polypeptide.

5. Claims: 14,16,18,28,48,54-61,66,77-82,
97 (all partially); 20,29 (completely)

A method of producing pantothenate (e.g., 2 g/L up to 40 g/L at least), e.g., in a manner independent of valine or alpha-ketoisovalerate feed, comprising culturing a microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*) or Gram-negative) having a deregulated isoleucine-valine (*ilv*) pathway, wherein the microorganism overexpresses acetohydroxyacid synthase or is transformed with a vector comprising an *ilvBN* nucleic acid sequence or an *alsS* sequence, e.g., from *Bacillus*, under conditions such that pantothenate is produced, and possibly further recovering the pantothenate. Said microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus* (e.g., *Bacillus subtilis*), *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*)), and said vector.

6. Claims: 14,16,18,28,48,54-61,66,77-82,
97 (all partially); 21,30 (completely)

A method of producing pantothenate (e.g., 2 g/L up to 40 g/L at least), e.g., in a manner independent of valine or alpha-ketoisovalerate feed, comprising culturing a microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*) or Gram-negative) having a deregulated isoleucine-valine (*ilv*) pathway, wherein the microorganism overexpresses acetohydroxyacid isomeroreductase or is transformed with a vector comprising an *ilvC* nucleic acid sequence, e.g., from *Bacillus*, under conditions such that pantothenate is produced, and possibly further recovering the pantothenate. Said microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus* (e.g., *Bacillus subtilis*), *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*)), and said vector.

7. Claims: 14,16,18,28,48,54-61,66,77-82,97 (partially); 22,
31 (completely)

A method of producing pantothenate (e.g., 2 g/L up to 40 g/L at least), e.g., in a manner independent of valine or alpha-ketoisovalerate feed, comprising culturing a microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci*

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

or Streptomyces) or Gram-negative) having a deregulated isoleucine-valine (ilv) pathway, wherein the microorganism overexpresses dihydroxyacid dehydratase or is transformed with a vector comprising an ilvD nucleic acid sequence, e.g., from Bacillus, under conditions such that pantothenate is produced, and possibly further recovering the pantothenate. Said microorganism (e.g., Gram-positive (e.g., belonging to the genus Bacillus (e.g., Bacillus subtilis), Corynebacterium, Lactobacillus, Lactococci or Streptomyces)), and said vector.

8. Claims: 25,28,50,54-61 (all partially)

A method of producing pantothenate (e.g., 2 g/L up to 40 g/L at least), e.g., in a manner independent of precursor feed, comprising culturing a microorganism (e.g., Gram-positive (e.g., belonging to the genus Bacillus, Corynebacterium, Lactobacillus, Lactococci or Streptomyces) or Gram-negative) having a mutant avtA gene under conditions such that pantothenate is produced, and possibly further recovering the pantothenate.

9. Claims: 25,28,50,54-61 (all partially)

A method of producing pantothenate (e.g., 2 g/L up to 40 g/L at least), e.g., in a manner independent of precursor feed, comprising culturing a microorganism (e.g., Gram-positive (e.g., belonging to the genus Bacillus, Corynebacterium, Lactobacillus, Lactococci or Streptomyces) or Gram-negative) having a mutant ilvE gene under conditions such that pantothenate is produced, and possibly further recovering the pantothenate.

10. Claims: 25,28,50,54-61 (all partially)

A method of producing pantothenate (e.g., 2 g/L up to 40 g/L at least), e.g., in a manner independent of precursor feed, comprising culturing a microorganism (e.g., Gram-positive (e.g., belonging to the genus Bacillus, Corynebacterium, Lactobacillus, Lactococci or Streptomyces) or Gram-negative) having a mutant ansB gene under conditions such that pantothenate is produced, and possibly further recovering the pantothenate.

11. Claims: 25,28,50,54-61 (all partially)

A method of producing pantothenate (e.g., 2 g/L up to 40 g/L at least), e.g., in a manner independent of precursor feed, comprising culturing a microorganism (e.g., Gram-positive (e.g., belonging to the genus Bacillus, Corynebacterium, Lactobacillus, Lactococci or Streptomyces) or Gram-negative)

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having a mutant *alsD* gene under conditions such that pantothenate is produced, and possibly further recovering the pantothenate.

12. Claims: 36,37,54-59,61 (all partially)

A method of producing beta-alanine, comprising culturing a microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*) or Gram-negative) which overexpresses an aspartate-alpha-decarboxylase-encoding gene, under conditions such that beta-alanine is produced, wherein the aspartate-alpha-decarboxylase-overexpressing microorganism has a mutation in a nucleic acid sequence encoding ketopantoate hydroxymethyltransferase (*panB*), and possibly further recovering the compound.

13. Claims: 36,37,54-59,61 (all partially)

A method of producing beta-alanine, comprising culturing a microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*) or Gram-negative) which overexpresses an aspartate-alpha-decarboxylase-encoding gene, under conditions such that beta-alanine is produced, wherein the aspartate-alpha-decarboxylase-overexpressing microorganism has a mutation in a nucleic acid sequence encoding ketopantoate reductase (*panE*), and possibly further recovering the compound.

14. Claims: 36,37,54-59,61 (all partially)

A method of producing beta-alanine, comprising culturing a microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*) or Gram-negative) which overexpresses an aspartate-alpha-decarboxylase-encoding gene, under conditions such that beta-alanine is produced, wherein the aspartate-alpha-decarboxylase-overexpressing microorganism has a mutation in a nucleic acid sequence encoding pantothenate synthetase (*panC*), and possibly further recovering the compound.

15. Claim : 38 (completely)

A method of producing beta-alanine comprising contacting a composition comprising aspartate with an isolated *Bacillus* aspartate-alpha-decarboxylase enzyme under conditions such that beta-alanine is produced.

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16. Claims: 41,44-47,51,53,54-61,69,71,72,75,78-81,
97 (all partially); 39,43,52,67,70,74,88-91,
108-110 (all completely)

A method for producing or for enhancing production of ketopantoate, pantoate, or pantothenate (e.g., 10, 20 or 40 g/L at least), comprising culturing a mutant microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*) or Gram-negative) having a mutant pantothenate kinase-encoding *coaX* gene, under conditions such that said panto-compound is produced or that production is enhanced, and possibly further recovering the compound. A method for identifying compounds which modulate pantothenate kinase activity comprising contacting a recombinant cell expressing the *coaX* gene, possibly further comprising a mutant *coaA* gene encoding a pantothenate kinase with reduced activity, with a test compound and determining the ability of the test compound to modulate pantothenate kinase activity in said cell. A recombinant microorganism having a mutant *coaX* gene encoding a pantothenate kinase with reduced activity. A vector comprising a mutant *coaX* gene encoding a pantothenate kinase with reduced activity, possibly further comprising regulatory sequences. A recombinant microorganism comprising a vector comprising an isolated *coaX* gene (e.g., from *Bacillus (subtilis)*), and said vector, possibly further comprising regulatory sequences, e.g., a constitutively active promoter. A recombinant microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus* (e.g., *Bacillus subtilis*), *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*)) that overproduces a panto-compound having a mutation in a *coaX* gene that results in a reduced level of pantothenate kinase activity, resulting in a decrease in the capacity of the microorganism to synthesize coenzyme A. An isolated nucleic acid molecule comprising a (mutant) *coaX* gene, and an isolated pantothenate kinase protein encoded by a *coaX* gene.

17. Claims: 41,44-47,51,53-61,69,71,72,75,78-81,
97 (all partially); 40,42,68,73 (all completely)

A method for producing or for enhancing production of a panto-compound, e.g., ketopantoate, pantoate or pantothenate (e.g., 10, 20 or 40 g/L at least), comprising culturing a mutant microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*) or Gram-negative) having a mutant pantothenate kinase-encoding *coaA* gene, under conditions such that the panto-compound is produced or that production is enhanced, and possibly further recovering the panto-compound. A recombinant microorganism having a mutant *coaA* gene encoding a pantothenate kinase with reduced

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activity. A recombinant microorganism (e.g., Gram-positive (e.g., belonging to the genus *Bacillus* (e.g., *Bacillus subtilis*), *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*)) that overproduces a panto-compound having a mutation in a *coaA* gene that results in a reduced level of pantothenate kinase activity, resulting in a decrease in the capacity of the microorganism to synthesize coenzyme A. A vector containing a (mutated) *coaA* gene.

18. Claim : 94 (partially)

A vector containing regulatory sequences comprising the constitutively active promoter Pveg (SEQ ID NO:41).

19. Claim : 94 (partially)

A vector containing regulatory sequences comprising the constitutively active promoter P15 (SEQ ID NO:39).

20. Claim : 94 (partially)

A vector containing regulatory sequences comprising the constitutively active promoter P26 (SEQ ID NO:40).

21. Claim : 96 (partially)

A vector containing regulatory sequences comprising an artificial RBS according to SEQ ID NO:49.

22. Claim : 96 (partially)

A vector containing regulatory sequences comprising an artificial RBS according to SEQ ID NO:50.

23. Claim : 96 (partially)

A vector containing regulatory sequences comprising an artificial RBS according to SEQ ID NO:51.

24. Claim : 96 (partially)

A vector containing regulatory sequences comprising an artificial RBS according to SEQ ID NO:52.

25. Claim : 96 (partially)

A vector containing regulatory sequences comprising an

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artificial RBS according to SEQ ID NO:53.

26. Claim : 96 (partially)

A vector containing regulatory sequences comprising an artificial RBS according to SEQ ID NO:54.

27. Claim : 96 (partially)

A vector containing regulatory sequences comprising an artificial RBS according to SEQ ID NO:55.

28. Claim : 96 (partially)

A vector containing regulatory sequences comprising an artificial RBS according to SEQ ID NO:56.

29. Claim : 96 (partially)

A vector containing regulatory sequences comprising an artificial RBS according to SEQ ID NO:57.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 00/25993

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